us-10-062-599-59.rag

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March 1, 2004, 16:36:28 ; Search time 54 Seconds (without alignments) 596.489 Million cell updates/sec
                                                                                                                                                                                                  1 MARGSLRRLLRLLVLGLWLA.....LSGFLVWRRCRRERSSPPPX 114
                                                                                                                                                                                                                                                                                                                        1586107
              Compugen Ltd
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compug
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                                                                   OM protein - protein search, using sw model
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608
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Perfect score:
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Minimum DB seq length: 0
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Maximum Match 100%
Listing first 45 summaries

Maximum Match 100%
Listing first 45 summar.

Database: A Geneseq 29Jan04:*
1: geneseqp1990s:*
2: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2001s:*
6: geneseqp2003ss:*
7: geneseqp2003ss:*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

geneseqp2004s:*

SUMMARIES

Description			Human	_	Human	Human		rung c	Human	7	3 TAT274	Aau79828 Mouse typ	Aau03500 Human TWE	Aav91463 Human sec		Human	Human	Human	Timer.	Human	Hullan	ь нишап	Aay91552 Human sec	Ada49370 Human Fnl	R TALL-1R	_	
π	AAW73409	AAW88506	AAY57940	AAU03498	ABP61512	AAU79827	ADA56889	ABU56716	ADC74112	ADD37867	ADD89033	44179828	ATT02500	2000000	AAISTAGS	ADA5/390	ADC/4462	ADD38025	AAY91604	ADA57391	ADC74463	ADD38026	22491552	00000	AUA495/0	ADBSOSES	ADB90665
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185 170 170 186 185 185 185 1380 1380 1881 1881 1844 1844 1844 1844 1844 18
0.000 0.000
97.5 96.5 96.5 97.5 99.5 99.5 99.5 99.5 99.5 99.5 99
77777777777777777777777777777777777777

ALIGNMENTS

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New isolated human genes - useful for diagnosis and treatment of, e.g. cancers, neurological disorders, immune diseases, developmental disorders
                                                                                          Secreted protein; human; protein therapy; gene therapy; blood disorder; pathological condition; diagnosis; cancer; neurological disorder; developmental abnormality; foetal deficiency; leukaemia; hepatic disease; immune system disorder; Alzheimer's disease; cognitive disorder; schizophrenia; prostate disease; autoimmune disorder; AlDS.
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                                                                                                                                                                                                                                                                                                                                                                                                              Endress GA,
                                                                                                                                                                                                    /note= "unspecified amino acid"
                                                                                                                                                                                                                                                                                                                                                                                                               Dillon PJ,
                                                                         Human secreted protein encoded by Gene No. 13.
                                                                                                                                                                                   Location/Qualifiers
                AAW73409 standard; protein; 114 AA
                                                                                                                                                                                                                                                                                                                                                                                                                Carter KĊ,
                                                                                                                                                                                                                                                                                                                     97US-0048150P.
97US-0048356P.
97US-0050935P.
                                                                                                                                                                                                                                                                                       97US-0044039P.
97US-0048093P.
97US-0048101P.
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97US-0056293P.
                                                                                                                                                                                                                                                                                                                                                                                            (HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                                                                                                                                                          97US-0056296P
                                                                                                                                                                                                                                                                    98WO-US010868
                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                   Rosen CA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1999-070209/06.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB; AAV08823.
                                                                                                                                                                                                                                                                                                                                                                                                              Ruben SM, Roser
                                                                                                                                                                                         Key
Misc-difference
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30-MAY-1997;
30-MAY-1997;
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                                                                                                                                                                                                                              WO9854206-A1
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                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                                                                                                                                        29-AUG-1997
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                                                                                                                                                                                                                                                                                                                                             30-MAY-1997
                                                                                                                                                                                                                                                                                                                                                                   29-AUG-1997
                                                                                                                                                                                                                                                   03-DEC-1998
                                                           19-FEB-1999
                                       AAW73409;
RESULT 1
AAW73409
ID AAW7
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New human proteins containing transmembrane domains and their encoding sequences - useful in the preparation of antibodies and large-scale protein production, gene diagnosis, and gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; Page 152-153; 178pp; English
          Claim 11; Page 153; 188pp; English
                                                                                                                                                                                                                                                                                                                                                                 Yamaguchi
                                                                                                                                                                                                                                                                                                                                                                             WPI; 1999-045730/04.
                                                                                                                                                                                                                                                                                                                                                                  Sekine S,
                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB; AAV84374.
or blood disorders.
                                                                                                                             Sequence 114 AA;
                                                                                                                                                                                                                                                                                                                                     03-JUN-1997;
                                                                                                                                                                                                                                                                                                  WO9855508-A2
                                                                                                                                                                                                                                                                                                                          03-JUN-1998;
                                                                                                                                                                                                                                                     30-MAR-1999
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                                                                                                                                                                                                                                          AAW88506;
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                                                                                                                                                                                                                                                                                                                                                                  Kato
                                                                                                                                                                                                                         AAW88506
                                                                                                                                                                                                                   RESULT
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ö This sequence is encoded by a cDNA of the invention, designated Gene No. 13. This sequence represents a human secreted protein, and is expressed protein, and is expressed in keratinocytes and to a lesser extent in endothelial cells and placenta. The DNA sequences of the invention and their corresponding secreted polypeptides are useful for preventing, treating or ameliorating medical conditions, e.g. by protein or gene therapy. Also pathological conditions can be diagnosed by determining the amount of the new polypeptides in a sample or by determining the presence of mutations in the DNA sequences. Specific uses are described for each of the DNA sequences and the encoded proteins, based on which tissues they are most highly expressed in, and include developing products for the diagnosis or treatment of cancer, tumours, neurological disorders, developmental diseases of the immune system (including allergies or asthma), hepatic disease, Alzheimer's and cognitive disorders, schizophrenia, prostate diseases, autoimmune disorders and AIDS. The polypeptides are also useful 9 9 designated Gene No 1 MARGSLRRILIRLIVLGLWLALLRSVAGEQAPGTAPCSRGSSWSADLDKCMDCASCRARPH 1 MARGSLRRLLRLLVLGLWLALLRSVAGEQAPGTAPCSRGSSWSADLDKCWDCASCRARPH Gaps tratement of cancer, tumours, neurological disorders, developmental abnormalities and foetal deficiencies, blood disorders, leukaemias, 61 SDFCLGCAAAPPAPFRLLWPILGGALSLTFVLGLLSGFLVWRRCRRERSSPPP . 0 Length 114; 0; Indels 99.8%; Score 607; DB 2; I 100.0%; Pred. No. 1.3e-55; 0; Mismatches for identifying their binding partners Matches 113; Conservative

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29-MAY-1998;
02-JUL-1998;
02-OCT-1998;
                                                                                                                                                                                                                                                                                                      W09961471-A2
                                                                                                                                                                                                                                                                                                                                                                      28-MAY-1999;
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                                                                                                 23-MAR-2000
                                                                                                                                                                                                                                                                                                                                      02-DEC-1999.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tang YT,
                                                               AAY57940;
RESULT 3
                                                                                                                                                                                                                                                                                              Human liver clone HP10432-encoded membrane protein.
                                                                                                                                                                                                                                                                                                                             Transmembrane protein; HP10432; human; liver.
                                                                                                                                                                                              AAW88506 standard; protein; 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (SAGA ) SAGAMI CHEM RES CENTRE (PROT-) PROTEGENE INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         97JP-00144948.
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AAZ56698 to AAZ56776 encode AAY57877 to AAY57955 which represent human

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0
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This is the amino acid sequence of a transmembrane protein encoded by human liver CDNA clone HP10432 (see AAV84374). The encoded protein has a signal-like N-terminal region and one internal transmembrane domain. The invention provides nucleotide sequences (see AAV84359-76) coding for 18 transmembrane proteins (see AAW8491-508), vectors containing such polymucleotides, and eukaryotic cells containing the vectors. The proteins can be used as antigens or as compositions in the preparation of antibodies against the proteins. The polymucleotides can be used as probes for gene diagnosis, and as gene sources for gene therapy and large-scale production of proteins encoded by the cDNA. The host cells are used for the detection of ligands corresponding to the expressed proteins, and the screening of low mol.wt. medicines
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Proteins, polynucleotides, vectors, host cells and antibodies used to diagnose, treat or prevent immune, reproductive, smooth muscle, neurological, gastrointestinal, developmental and cell proliferative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human, transmembrane protein; HTMPN; diagnosis; immunospecific; antiproliferative; neuroprotective; immune disorder; reproductive disorder; smooth muscle disorder; neurological disorder; gastrointestinal disorder; developmental disorder;
                                                                                                                                                                                                                                                                                                       1 MARGSLRRLLRLLVLGLWLALLRSVAGEQAPGTAPCSRGSSWSADLDKCMDCASCRARPH
                                                                                                                                                                                                                                                                                                                                 1 MARGSLRRILRLVIGIMLALIRSVAGEQAPGTAPCSRGSSWSADLDKCMDCASCRARPH
                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                     SDFCLGCAAAPPAPFRLLWPILGGALSLTFVLGLLSGFLVWRRCRRERSSPPP 113
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Baughn MR,
                                                                                                                                                                                                                                            Length 129;
                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Guegler KJ,
Kaser MR, E
                                                                                                                                                                                                                                            Score 571; DB 2; L
Pred. No. 8.4e-52;
0; Mismatches 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lal P, Hillman JL, Yue H,
, Patterson C, Gorgone GA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human transmembrane protein HTMPN-64.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; Page 163; 229pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAY57940 standard; protein; 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     98US-0087260P.
98US-0091674P.
98US-0102954P.
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                                                                                                                                                                                                                                                 93.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cell proliferative disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
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                                                                                                                                                                                                                                                                                 Matches 107; Conservative
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                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
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                                                                                                                                                                                                                     Sequence 129 AA;
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              transmembrane protein have immunospecific, antiproliferative and neuroprotective activities. The human transmembrane proteins, polynucleorides encoding them and other compositions and methods from the present invention, can be used for the diagnosis, treatment or prevention of immune, reproductive, smooth muscle, neurological, gastrointestinal, to treat or prevent disorders associated with a decreased expression or activity of HTMPN
                                                                                                                                                                                                                                                 1 MARGSLRRLLRLLVLGLWIALLRSVAGEQAPGTAPCSRGSSWSADLDKCMDCASCRARPH 60
                                                                                                                                                                                                                                                                                  9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ocular neovascularisation; diabetic retinopathy; neovascular glaucoma; retinoblastoma; retinopathy of prematurity; retrolental fibroplasia; rubeosis; uveitis; macular degeneration; arthritis; rheumatism; corneal graft neovascularisation; psoriasis; metastatic condition; malignant tumour; sarcoma; carcinoma; benign tumour; haemophilic joint; preneoplastic condition; myocardial angiogenesis; wound granulation; scleroderma; vascular adhesion; telangiectasia; ischaemia; human;
                                                                                                                                                                                                                                                                                  1 MARGSLRRLLRLLVLGLWLALLRSVAGEQAPGTAPCSRGSSWSADLDKCMDCASCRARPH
transmembrane proteins designated HTMPN-1 to HTMPN-79, respectively.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               atherosclerotic plague neovascularisation; coronary atherosclerosis;
                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      receptor; TWEAKR; tumour necrosis factor; TNF; angiogenesis;
                                                                                                                                                                                                                                                                                                                 SDFCLGCAAAPPAPFRLLWPILGGALSLTFVLGLLSGFLVWRRCRRERSSPPP 113
                                                                                                                                                                                                                                                                                                                                        61 SDFCLGCAAAPPAPFRLLWPILGGALSLTFVLGLLSGFLVWRRCRRREKFTTP 113
                                                                                                                                                                                                                       ;
                                                                                                                                                                                          Length 129;
                                                                                                                                                                                                                       Indels
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                                                                                                                                                                                        Score 571; DB 3;
Pred. No. 8.4e-52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'note= "Extracellular domain"
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                                                                                                                                                                                                                       0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human TWEAK receptor (TWEAKR) polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note= "Signal peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                             AAU03498 standard; protein; 129 AA
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                                                                                                                                                                                        93.9%;
Local Similarity 94.7%;
tes 107; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   peripheral atherosclerosis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
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                                                                                                                                                            Sequence 129 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO200145730-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26-SEP-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAU03498;
                                                                                                                                                                                                                                                                                                                      61
                                                                                                                                                                                           Query Match
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Domain
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Matches
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TWEAK protein is a member of the tumour necrosis factor (TNF) family and induces angiogenesis. TWEAKR may therefore be used to screen for and develop TWEAKR agonists and antagonists for the modulation of angiogenesis. TWEAKR may therefore be used to screen for and develop TWEAKR agonists and antagonists for the modulation of angiogenesis, to be used in the treatment and diagnosis of human disease. The disorders mediated by angiogenesis include ocular disorders characterised by ocular neovascularisation such as diabetic retinopathy, neovascular glaucoma, retinopathy of prematurity, cretrolental fibroplasia, rubeosis, uveitis, macular degeneration and correlation and profit and provascularisation, and inflammatory diseases such as arthritis, rheumatism and psoriasis. Other treatable diseases include anthorizing and metastatic conditions such as sarcomas and carcinomas, malignant and metastatic conditions, myocardial angiogenesis, chaemophilic joints, scleroderma, vascular adhesions, atherosclerotic plaque neovascularisation, telangiectasia, wound granulation, coronary contary atherosclerosis, peripheral atherosclerosis and ischaemia
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9
                                              Modulating angiogenesis in a mammal for treating diseases mediated by angiogenesis, e.g. solid tumors and vascular deficiencies of cardiac or peripheral tissue, by administering antagonist or agonist of TWEAK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MARGSLRRILRILVIGIMLALLRSVAGEQAPGTAPCSRGSSWSADLDXCMDCASCRARPH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; NF-kB; nuclear factor kappa B; mouse; antiinflammatory; immunomodulator; cytostatic; antiinfective; osteopathic; nootropic; neuroprotective; anti-HIV; autoimmune disease; cancer; infection; bone disease; AIDS; neurodegenerative disease; ischaemic disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 SDFCLGCAAAPPAPFRLLWPILGGALSLTFVLGLLSGFLVWRRCRRERSSPPP 113
                                                                                                                                                                                      represents the human TWEAK receptor (TWEAKR) protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 SDFCLGCAARPAAPFRLIMPILGGALSLTFVLGLLSGFLVWRRCRREKFTTP 113
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              93.9%; Score 571; DB 4; 94.7%; Pred. No. 8.4e-52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nagano Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human NF-kB activating protein SEQ ID NO 178.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
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                                                                                                                                                       Example 1; Fig 1; 46pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28-DEC-2000; 2000JP-00402288.
26-MAR-2001; 2001JP-00088912.
24-AUG-2001; 2001JP-00254018.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25-DEC-2001; 2001WO-JP011389.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (ASAH ) ASAHI KASEI KOGYO KK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 94.7
Matches 107; Conservative
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2001-417975/44.
                N-PSDB; AAS03963.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 129 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30-SEP-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matsuda A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABP61512;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 5
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Methods of modulating angiogenesis and inhibiting tumor progression,
                                                                                                                                                                                                                                                                                                                                                   Disclosure; Fig 10A; 37pp; English.
                                                                                                                                                                                                                                                                                                                                         using TWEAK receptor agonists
                                                                                                                Matches 107; Conservative
                                                                                                                                                                                                                                                                                                                  Browning J, Burkly L,
                                                                                                                                                                                                                                                                                                                            WPI; 2002-383103/41
                            diseases and cancer.
2002-583617/62
                                                                                                                                                                                                                                                                                                         BIOJ ) BIOGEN INC
                                                                                             Sequence 129 AA;
     N-PSDB; ABQ92000
                                                                                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                                            21-MAR-2002
                                                                                                                                                                                                  15-JUL-2002
                                                                                                       Query Match
                                                                                                                                                                                       AAU79827
                                                                                                            Local
                                                                                                                                                                     RESULT 6
                                                                                                                                                                         AAU79827
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Similarity

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The invention describes methods of modulating angiogenesis and inhibiting tumour progression using TWEAK (a novel member of the tumour necrosis factor or TWF family) receptor agonists. Conditions which can be treated using the agonists include myocardial ischaemic conditions (e.g. myocardial infarction), wound healing (e.g. burn healing and healing of gastric ulcers), and tissue and organ transplanteations to promote neovascularisation, particularly in subjects suffering from vascular insufficiency (e.g. diabetic patients). Inhibition of angiogenesis and subsequently neovascularisation is useful in treatment of cancer, inflammatory macular degeneration and diabetic retinopathy. This sequence represents the human type I transmembrane protein Fn14, a TWEAK receptor described in the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cytostatic; cerebroprotective; neuroprotective; nootropic; cardiovascular; antiarteriosclerotic; gene therapy; cardiovascular; antiarteriosclerotic; gene therapy; neuroprotective; noterapy; neuroprotective; noterapy; new secreted protein; immune disorder; inflammation; respiratory disorder; cancer; CNS disorder; neurodegenerative disorders; inflammatory bowel disease; nephritis; Crohn's disease; asthma; allergy; multiple solerosis; achteroslerosis; myocarditis; chromosome mapping; triple helix formation; antisense gene therapy; forensic biology.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MARGSLRRILLRILVIGIWIALIRSVAGEQAPGTAPCSRGSSWSADLDKCMDCASCRARPH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MARGSLRRILIRILVIGIWLALIRSVAGEQAPGTAPCSRGSSWSADLDKCMDCASCRARPH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 SDFCLGCAAAPPAPFRLLWPILGGALSLTFVLGLLSGFLVWRRCRRERSSPPP 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 SDFCLGCAAAPPAPFAFFILWPILGGALSLTFVLGLLSGFLVWRRCRREKFTTP 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      immunosuppressive; antiinflammatory; antiasthmatic; antiallergic;
                                                                                                                                                                                                                                                                                                                                                                                                            Length 129;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                IndelB
                                                                                                                                                                                                                                                                                                                                                                                                         93.9%; Score 571; DB 5;
94.7%; Pred. No. 8.4e-52;
Live 0; Mismatches 6
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19-JUL-2001; 2001US-0306171P.
13-NOV-2001; 2001US-0331287P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human secreted protein #172.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 94.7
Matches 107; Conservative
                                                                                                                                                                                                                                                                                                                                                                Sequence 129 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO2002102994-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
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                                                                                                                                                                                                                                                       The invention relates to a purified protein (I), comprising one of 90 fully defined sequences (ABP61424-ABP61513) or a protein based on any of the sequences but with some amino acids deleted, substituted or added and with a NF-kB (nuclear factor kappa B) activating effect. The protein and encoding gene (ABC91912-ABC92001) are useful in diagnosis and screening inhibitors or prometers to control excessive activation or inhibition and for treating e.g. inflammations, autolimmume diseases, cancers, inflammations, autolimmume diseases, cancers, inflammations, hone diseases, AIDS, neurodegenerative diseases or ischaemic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            tumour progression;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MARGSLRRLLRLLVLGLWLALLRSVAGEQAPGTAPCSRGSSWSADLDKCMDCASCRARPH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Type 1 transmembrane protein Fn14; human; cytostatic; cardiant; vulnerary; TWEAK agonist; Fn14 agonist; angiogenesis; tumour progress tumour necrosis factor family; TNF family; TWEAK receptor; myocardial ischaemic condition; myocardial infarction; wound healing; burn healing; gastric ulcer; tissue transplantation; organ transplantation; necovascularisation; vascular insufficiency; cancer; inflammatory macular degeneration; diabetic retinopathy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MARGSLRRILIRLIVLGLWLALLRSVAGEQAPGTAPCSRGSSWSADLDKCMDCASCRARPH
                                                                          NF-approximatelykB activating gene and expressed protein, applicable diagnosis and screening inhibitors or promoters to control excessive activation or inhibition for treating e.g. inflammations, autoimmune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 SDFCLGCAAAPPAPPRLLWPILGGALSLTFVLGLLSGFLVWRRCRRERSSPPP 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 129;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 93.9%; Score 571; DB 5; Length 12:
94.7%; Pred. No. 8.4e-52;
ive 0; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human type 1 transmembrane protein Fn14.
                                                                                                                                                                                                                 Claim 4; Page 814-815; 841pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAU79827 standard; protein; 129 AA
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New human secreted polypeptides and polymucleotides, useful for diagnosing, treating or preventing e.g. immune disorders, inflammatory conditions, respiratory disorders, cancers, CNS disorders, or neurodegenerative disorders.

Rosen CA, Ruben SM; WPI; 2003-167512/16. N-PSDB; ADA55993.

Zheng T;

Jakubowski A,

ò

Gaps

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us-10-062-599-59.rag

ß

The invention relates to 592 new human secreted polypeptides useful for Claim 13; SEQ ID NO 1079; 1754pp; English

the invention teletes to 59% new numan secreted polypeptides useful for diagnosing, treating or preventing e.g. immune disorders, inflammatory conditions, respiratory disorders, cancers, CNS disorders, or neurodegenerative disorders, or polypeptides comprising an amino acid sequence at least 95% identical to the new sequences. The polypeptides, catids encoding the polypeptides, agonists or antagonists that binds to the polypeptides are useful in preparing diagnostic or pharmaceutical compositions for diagnosing, treating diagnostic or pharmaceutical compositions for diagnosing, treating of preventing an e.g. immune disorders (e.g. gastric, ovarian or lung cancer), CNS disorders (e.g. multiple sclerosis or ischaemic brain injury), neurodegenerative cardiovascular disorders (e.g. atherosclerosis or myocarditis). The collymolectides are useful for chromosome identification, chromosome or antisense DNA or RNA, in gene therapy, for identifying individuals from minute biological samples, in forensic biology, and as hybridization probes. The polypeptides are useful for as molecular weight markers on sodium dodecyl sulface-polyacrylamide gel electrophoresis (SDS-PAGE) gels, to raise antibodies, for testing biological activities, and for treating or preventing neural disorders, immune system disorders, muscular, reproductive, gastrointestinal, pulmonary, cardiovascular, renal, proliferative and/or cancerous diseases. This sequence corresponds to one of the polypeptide of the invention. Note: The sequence data for this patent did form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences

Sequence 129 AA;

1 MARGSIRRILIRILVIGIMLALIRSVAGEQAPGTAPCSRGSSWSADLDKCMDCASCRARPH 60 1 MARGSLRRILRILVIGIMIALIRSVAGEQAPGTAPCSRGSSWSADLDKCMDCASCRARPH 60 Gaps SDFCLGCAAAPPAPFRLLWPILGGALSLTFVLGLLSGFLVWRRCRRERSSPPP 113 ó 93.9%; Score 571; DB 6; Length 129; 94.7%; Pred. No. 8.4e-52; ive 0; Mismatches 6; Indels Conservative Similarity Matches 107; 61 Query Match Local ò g ð

ABUS6716 standard; protein; 129 AA ABU56716 RESULT

(first entry) 02-APR-2003 ABU56716;

Lung cancer-associated polypeptide; cytostatic; emphysema; atelectasis; antiinflammatory; antiasthmatic; non-small cell lung cancer; atelectasis; small cell lung cancer; benign lession; precancerous lesion; bronchitis; chronic obstructive pulmonary disease; hypersensitivity pneumonitis; interstitial pulmonary fibrosis; fibrosis; asthma; bronchiectasis. Lung cancer-associated polypeptide #309.

Unidentified

W0200286443-A2

31-OCT-2002

18-APR-2002; 2002WO-US012476.

18-APR-2001; 2001US-0284770P. 10-MAY-2001; 2001US-0290492P.

The invention relates to a method for detecting a lung cancer-associated transcript in a cell from a patient, comprising contacting a biological transcript in a cell from a patient, comprising contacting a biological sample from the patient with a polymucleotide that selectively hybridises to a sequence that is at least 80 % identical to a gene that exhibits concerned or decreased expression in lung cancer samples. Lung cancer samples compound that modulates a lung cancer-associated polypeptide, for compound that modulates a lung cancer-associated polypeptide, for cancer in a patient and for treating a mammal having lung cancer by administering a modulatory compound identified. The methods are useful for treating lung cancer, such as small cell lung cancer, non-small cell for treating lung cancer or precancerous leasions, e.g. attenderasis, emphysema, bronchitis, chronic obstructive pulmonary disease, fibrosis, chypersensitivity pneumonitis, interstitial pulmonary disease, is asthma and bronchiectasis. The genes, polymucleotides and polypeptides are useful for diagnostic purposes and as targets for screening for therapeutic compounds that modulate lung cancer, such as antibodies. Sequences Detecting a lung cancer-associated transcript in a cell from a patient for treating lung cancer, by contacting a biological sample from the patient with a polynucleotide that exhibits increased or decreased expression in lung cancer. Claim 27; Page 429; 453pp; English (EOSB-) EOS BIOTECHNOLOGY INC. 09-NOV-2001; 2001US-0339245P. 13-NOV-2001; 2001US-0350666P. 29-NOV-2001; 2001US-0334370P. 12-APR-2002; 2002US-0372246P. WPI; 2003-093161/08. Aziz N, Murray R; Sequence 129 AA; N-PSDB; ABX76445 nvention

09 Gaps ö 107; Conservative Similarity Query Match Best Local S Matches

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9 1 MARGSLRRILIRLIVLGIWLALLRSVAGEQAPGTAPCSRGSSWSADLDKCMDCASCRARPH SDFCLGCAAAPPAPFRLLWPILGGALSLTFVLGLLSGFLVWRRCRRERSSPPP 61 SDFCLGCAAAPPAPFRLLWPILGGALSLTFVLGLLSGFLVWRRCRREKFTTP 61 ð 셤 ò ద

ADC74112 standard; protein; 129 AA. ADC74112; RESULT 9 ADC74112

(first entry)

01-JAN-2004

Human secreted protein - SEQ ID 745.

antianaemic, antirheumatic, antiarthritic; antiinflammatory, antithyroid, antidabetic, immunosuppressive, dermatological; nephrotropic; antiparkinsonian; neuroprotrective, nootropic, antibacterial; virucide; fungicide, antiparasitic, antiarteriosclerotic; vulnerary; cytostatic; haemopoietic, haematologic, anaemia; autoimmune disorder; rheumatoid arthritis; inflammation; Grave's disease; diabetes; systemic lupus erythematosus; glomerulonephritis; neurodegenerative; parkinson's; Alzheimer's; wound; hyperproliferative; atherosclerosis; cancer; bacterial; viral; fungal; parasitic infection; gene therapy;

New human secreted proteins and nucleic acid molecules, useful for preparing a diagnostic or pharmaceutical composition for diagnosing or treating allergic or asthmatic disorders, or related immediate

21-MAR-2001; 2001US-0277340P. 19-JUL-2001; 2001US-0306171P. 13-NOV-2001; 2001US-0331287P.

19-MAR-2002; 2002WO-US008279

WO200290526-A2 Homo sapiens.

14-NOV-2002

(HUMA-) HUMAN GENOME SCI INC.

Ruben SM;

Rosen CA,

WPI; 2003-140218/13

Claim 1; SEQ ID NO 349; 1323pp; English

hypersensitivity disorders

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New human secreted polypeptide for diagnosing, preventing or treating hematopoietic or hematologic disorders (e.g. anemia), autoimmune disorders (e.g. diabetes) or hyperproliferative disorders (e.g. cancer or atherosclerosis).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               human secreted protein; Antiallergic; Antiinflammatory; Antibacterial;
Anti-HIV; Cytostatic; Immunosuppressive; Hemostatic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADD37867 standard; protein; 129 AA
                                                                                          19-JUL-2001; 2001US-0306171P.
                                                                   19-MAR-2002; 2002WO-US008277
                                                                                   21-MAR-2001; 2001US-0277340P
                                                                                                                    (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human secreted protein #50
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                                                                                                                                                     WPI; 2003-430516/40.
N-PSDB; ADC73497.
                                                                                                                                     Rosen CA, Ruben SM;
                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                            Sequence 129 AA;
                                 WO2003038063-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15-JAN-2004
                 Homo sapiens
                                                  08-MAY-2003
                                                                                                                                                                                                                                                                                                                                                                            invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADD37867;
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                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
human.
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                                                                                                                                                                                                                                           haemopoietic or haemacologic disorder such as anaemia, autoimmune disorders such as rheumatoid arthritis, inflammation, Grave's disease, diabetes such as rheumatoid arthritis, inflammation, Grave's disease, diabetes, systemic lupus erythematosus or glomerulonephritis, neurodegenerative disorders including Parkinson's disease and Alzheimer's disease, wounds and hyperproliferative disorders including atherosclerosis or cancer, as well as bacterial, viral, fungal or parasitic infections. The polypeptide may also be used during-gene the polypeptide with a binding partner and determining whether the binding partner increases or decreases the activity of the polypeptide. The current sequence is that of the human secreted protein of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MARGSLRRLLRLLVLGLWLALLRSVAGEQAPGTAPCSRGSSWSADLDKCMDCASCRARPH 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9
                                                                       The invention relates to a novel human secreted polypeptide comprising defined sequence given in the specification. The polypeptide, nucleic acid molecule, antibody, agonist or antiagonist of the invention may be useful for preparing a composition for diagnosing or treating a haemopoletic or haematologic disorder such as anaemia, autoimmune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MARGSIRRIIRLIVLGLWLALIRSVAGEQAPGTAPCSRGSSWSADLDKCMDCASCRARPH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
Claim 16; SEQ ID NO 745; 2272pp; English.
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The present invention relates to an isolated polypeptide or human secreted protein. The polypeptides, nucleic acid molecules, antibodies or their fragmentes, and agonists or antigonists that bind are useful for preparing a diagnostic or pharmaceutical composition for diagnosting or treating allergic or asthmatic disorders. The polypeptide is also useful cor their fighting partner by contexting the polypeptide with a binding partner, and determining whether the binding partner increases to binding partner are also useful for detecting, preventing, diagnosing, prognosticating, treating or ameliocrating inflammatory disorders compastic diseases, wound healing and disorders of epithelial cell composition immune disorders, cardiovascular disorders blood-related disorders. The nucleic acids are also useful for chromosome context infectious diseases, endocrine disorders, or gastrointestinal disorders. The nucleic acids are also useful for chromosome contential and markers, or as hybridization or diagnostic probes. The polypeptides and antibodies are useful for providing immunological probes for differential identification of the tissues immunological probes for differential identification of the tissues immunological probes for differential identification a human contents a human contents and antibodies are useful.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Immunohistochemistry assays. The present sequence represents a human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            tumour-associated antigenic target polypeptide; Cytostatic; tumour;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 SDFCLGCAAAPPAPFRLLMPILGGALSLTFVLGLLSGFLVWRRCRREKFTTP 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ő
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              93.9%; Score 571; DB 7; Length 129; 94.7%; Pred. No. 8.4e-52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADD89033 standard; protein; 129 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    94.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 94.7'
Matches 107; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            secreted protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 129 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      29-JAN-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADD89033;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TAT274.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 11
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cancer

2002WO-US041798

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The present invention relates to antibodies against tumour-associated antigenic target polypeptide. The antibody is useful for treating or diagnosing tumours or cancers in mammals, e.g. prostate cancer, lung cancer, breast caner, colon cancer, ovarian cancer, prostate adenocarcinomas, renal cell carcinomas, or pleural mesothelioma. The present sequence represents a TAT polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MARGSLRRLLRLLVLGLWLALLRSVAGEQAPGTAPCSRGSSWSADLDKCMDCASCRARPH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MARGSLRRILRLIVLGLWIALLRSVAGEQAPGTAPCSRGSSWSADLDKCMDCASCRARPH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              vulnerary; TWEAK agonist; Fn14 agonist; angiogenesis; tumour progress: tumour necrosis factor family; TNF family; TWEAK receptor; myocardial ischaemic condition; myocardial infarction; wound healing; burn healing; gastric ulcer; tissue transplantation; organ transplantation; neovascularisation; vascular insufficiency; cancer; inflammatory macular degeneration; diabetic retinopathy.
                                                                                                                                                                                                                                                                                                                                                                                                                             New antibodies against tumor-associated antigenic target polypeptide, useful for treating or diagnosing tumors or cancers in mammals, e.g. prostate cancer, lung cancer, prostate adenocarcinomas or renal cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SPFCLGCAAAPPAPFRLLWPILGGALSLTFVLGLLSGFLVWRRCRREKFTTP 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SDFCLGCAAAPPAPFRLLWPILGGALSLTFVLGLLSGFLVWRRCRRERSSPPP 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Type 1 transmembrane protein Fn14; mouse; cytostatic; cardiant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mouse type 1 transmembrane protein Fn14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; SEQ ID NO 37; 252pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAU79828 standard; protein; 129
                                                                                                                                       2002US-0345444P.
2002US-0351885P.
2002US-0360066P.
2002US-0362004P.
2002US-0366869P.
                                                                                                                                                                                                                     2002US-0366284P.
2002US-0368679P.
2002US-0404809P.
2002US-0405645P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 94.7
Matches 107; Conservative
                                                                                                                                                                                                                                                                                                                                   Hillan KJ,
                                                                                                                                                                                                                                                                                                     (GETH ) GENENTECH INC
                                                                                                                                                                                                                                                                                                                                                                                    2003-569537/53.
                                                                                                                                                                                                                                                                                                                                                                                                    N-PSDB; ADD89109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 129 AA;
                                              WO2003057160-A2
                                                                                                                                                                                                                     21-MAR-2002;
28-MAR-2002;
19-AUG-2002;
21-AUG-2002;
                                                                                                            30-DEC-2002;
                                                                                                                                                                                                                                                                                                                                                      Williams PM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15-JUL-2002
                                                                                                                                                                                       05-MAR-2002;
                  Homo sapiens
                                                                                                                                                            25-JAN-2002;
                                                                                                                                                                          25-FEB-2002;
                                                                                                                                                                                                        20-MAR-2002;
                                                                                                                                            02-JAN-2002;
                                                                            17-JUL-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   carcinomas
                                                                                                                                                                                                                                                                                                                                     Frantz G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAU79828;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
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tumour progression using TWEAK (a novel member of the tumour necrosis factor or TNF family) receptor agonists. Conditions which can be treated using the agonists include myocardial ischaemic conditions (e.g. myocardial infarction), wound healing (e.g. burn healing and healing of gastric ulcers), and tissue and organ transplantations to promote neovascularisation, particularly in subjects suffering from vascular insufficiency (e.g. diabetic patients). Inhibition of angiogenesis and subsequently neovascularisation is useful in treatment of cancer, inflammatory macular degeneration and diabetic retinopathy. This sequence represents the mouse type I transmembrane protein Ful4, a TWEAK receptor
                                                                                                                                                                                                                                                                                                                                                                                                                The invention describes methods of modulating angiogenesis and inhibiting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ocular neovascularisation, diabetic retinopathy, neovascular glaucoma, retinoblastoma, retinopathy of prematurity, retrolental fibroplasia, rubeosis, uveitis, macular degeneration, arthritis, rheumatism, corneal graft neovascularisation, psoriasis, metastatic condition, malignant tumour, sarcoma, carcinoma, benign tumour, haemophilic joint, preneoplastic condition, myocardial angiogenesis, wound granulation, scleroderma, vascular adhesion, telangiectasia, ischemia, human, atherosclerotic plaque neovascularisation; coronary atherosclerosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MARGSLRRILELLVLGLWLALLRSVAGEQAPGTAPCSRGSSWSADLDKCMDCASCRARPH
                                                                                                                                                                                                                                                                                                                 Methods of modulating angiogenesis and inhibiting tumor progression,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 SDFCLGCAAADPAHFRLLWPILGGALSLVLVLALVSSFLVWRRCRRREKFTTP 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TWEAK receptor; TWEAKR; tumour necrosis factor; TNF; angiogenesis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        peripheral atherosclerosis; human IgG1; TWEAKR-Fc; fusion protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 SDFCLGCAAAPPAPFRILIWPILGGALSLTFVLGLLSGFLVWRRCRRERSSPPP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human TWEAK receptor-Fc (TWEAKR-Fc) fusion polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      74.0%; Score 450; DB 5; 75.2%; Pred. No. 3.8e-39; tive 6; Mismatches 22.
                                                                                                                                                                                                                                         Zheng T;
                                                                                                                                                                                                                                             Jakubowski A,
                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Fig 10B; 37pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAU03500 standard; protein; 309 AA
                                                                                                                                                                                                                                                                                                                                       using TWEAK receptor agonists
                                                                                                                           12-SEP-2001; 2001WO-US028451.
                                                                                                                                                                 14-SEP-2000; 2000US-0232355P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              described in the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                85; Conservative
                                                                                                                                                                                                                                             Browning J, Burkly L,
                                                                                                                                                                                                                                                                               WPI; 2002-383103/41
                                                                                                                                                                                                     (BIOJ ) BIOGEN INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 129 AA;
                                                   WO20022166-A2
               Mus musculus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         26-SEP-2001
                                                                                       21-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAU03500;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local
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Spencer SD;

Smith V,

Phillips H, Polakis P, Zhang Z;

Wu TD,

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Gaps

9 9

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Gaps

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Length 129; Indels

Score 571; DB 7; L. Pred. No. 8.4e-52; 0; Mismatches 6;

93.9%;

09 9 Homo sapiens.

tumour progression;

(first entry)

Synthetic.

AAY91463 standard; protein; 112 AA.

RESULT 14

AAY91463

/note= "From TWEAKR extracellular domain. Specifically referred to in Claims 4 and 10"

/note= "From a BglII cloning site"

. 81

82. .309 /note= "Fc portion"

/note= "Mature human TWEAKR-Fc fusion protein. Specifically referred to in Claim 11"

'note= "Signal peptide"

309

Location/Qualifiers

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The sequence represents a fusion protein consisting of the human TWEAK receptor (TWEAKR) protein extracellular domain fused to an Fc portion from human 1961. This fusion protein, TWEAKR-Fc, is used in the preparation of TWEAKR agonists and antagonists. The TWEAK protein is a majogenesis. TWEAKR may therefore be used to screen for and develop TWEAKR agonists and antagonists for the modulation of angiogenesis, to be used in the treatment and diagnosis of human disease. The disorders canding angiogenesis include ocular disorders characterised by onclar neovascularisation such as diabetic retinopathy, neovascular glaucoma, retinopathy of prematurity, retrolental fibroplasia, retinopathy of prematurity, retrolental fibroplasia, cubeosis, uveitis, macular degeneration and corneal graft neovascularisation, and inflammatory diseases such as arthritis, cheumatism and psoriasis. Other treatable diseases include malignant and metastatic conditions such as sarcomas and carcinomas, benign tumours and prematurine and prematicular allegal angiogenesis, haemophilic joints, conditions autheriosclerotic plaque.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Modulating angiogenesis in a mammal for treating diseases mediated by angiogenesis, e.g. solid tumors and vascular deficiencies of cardiac or peripheral tissue, by administering antagonist or agonist of TWEAK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    neovascularisation, telangiectasia, wound granulation, coronary atherosclerosis, peripheral atherosclerosis and ischaemia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 4; Page 45-46; 46pp; English
                                                                                                                                                                                                                                                                                                                                                                         20-DEC-1999; 99US-0172878P.
10-MAY-2000; 2000US-0203347P.
                                                                                                                                                                                                                                                                                                                                     19-DEC-2000; 2000WO-US034755
                                                                                                                                                                                                                                                                                                                                                                                                                             (IMMV ) IMMUNEX CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2001-417975/44.
N-PSDB; AAS03965.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 309 AA;
                                                                                                                                                                                                                                                                  NO200145730-A2
                                                                                                                                                                                                                                                                                                     28-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Wiley SR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local S
                                                                       Protein
                                   Peptide
                                                                                                                         Domain
                                                                                                                                                                             Region
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The polynucleotide sequences given in AAA26346 to AAA26458 encode the human secreted proteins given in AAY91451 to AAY91691. The human secreted proteins given in AAY91451 to AAY91691. The human secreted proteins can have activities based on the tissues and cells they are expressed in. Examples of the activities are: cytostatic; they are influenced in munosuppressive; antifary antiantlammatory; nootropic; neuroprotective; antialergic; osteopathic; antiarthritic; antibacterial; antidiabetic; antiathma; antipsoriatic; and cardiant. The polynucleotides and their corresponding secreted proteins are useful for preventing, treating or ameliorating medical conditions, e.g. by protein or gene therapy. Also pathological conditions can be diagnosed by determining the amount of the polynucleotides. Specific uses are described for each of the colynucleotides, based on which tissues they are most highly expressed in, and include developing products for the diagnosis or treatment of cancer, tumours, neurodegenerative disorders, diseases of the immune system, autoimmune diseases, hepatic and renal diseases of the immune system, autoimmune diseases, hepatic and renal disease, inflammation, allergies, arthritis, infections, AlbS, spinal cord injuries, insection, allergies, arthritis, infections, AlbS, spinal cord injuries, insection,
                                                                                                                                   Human; secreted protein; diagnosis; cytostatic; immunosuppressive; antiHIV; antiinflammatory; nootropic; neuroprotective; antiallergic; osteopathic; antiarthritic; antibacterial; antidiabetic; antiasthma; antipsoriatic; cardiant; gene therapy; cancer; neurological disorder; immune disease; inflammation; blood disorder; tumour; chromosome 16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New isolated human genes and the secreted polypeptides they encode, useful for diagnosis and treatment of e.g. cancers, neurological disorders, immune diseases, inflammation or blood disorders.
                                                                                           Human secreted protein sequence encoded by gene 13 SEQ ID NO:136.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Komatsoulis GA, Rosen CA, Ruben SM, Duan R, Moore PA,
Lafleur D, Wei Y, Ni J, Florence KA, Young PE, Brewer
Soppet DR, Endress GA, Ebner R, Olsen HS, Mucenski M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 11; Page 465; 634pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                      98US-0094657P.
98US-0095486P.
98US-0095454P.
98US-0095455P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                                                                                                                                                                  99WO-US017130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  98US-0096319P
                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lafleur D, Wei Y, Ni J,
Soppet DR, Endress GA, F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2000-195282/17.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-PSDB; AAA26358
                                                                                                                                                                                                                                                                                                    WO200006698-A1.
                                                                                                                                                                                                                                                             Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                  29-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12-AUG-1998;
                                                         29-JUN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                           05-AUG-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                06-AUG-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 06-AUG-1998;
                                                                                                                                                                                                                                                                                                                                          10-FEB-2000,
                   AAY91463;
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diabetes, asthma, sepsis, acne, psoriasis, cardiovascular disorders, reproductive disorders, gastrointestinal disorders, respiratory disorders and metabolic disorders. The proteins or polynucleotides can also be used

22;

71.2%; Score 433; DB 4; Length 309; 74.1%; Pred. No. 5.7e-37; cive 2; Mismatches 5; Indels

2; Mismatches

83; Conservative

Matches

g ð

Similarity

61 SDFCLGCAAAPPAPFRLLWPILGGALSLTFVLGLLSGFLVWRRCRRERSSPP 112

SDFCLGCAAAPPAPFRLL-----

----WRSCDKTHICPP 90

as food additives or preservatives. The proteins are also useful for identifying their binding partners. AAA26337 to AAA26345 and AAY91450 are sequences used in the exemplification of the present invention

Sequence 112 AA;

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Gaps

1;

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inflammatory bowel disease; nephritis; Crohn's disease; asthma; allergy; multiple sclerosis; ischaemic brain injury; Parkinson's disease; Alzheimer's disease; atherosclerosis; myocarditis; chromosome mapping; triple helix formation; antisense gene therapy; forensic blology.
                                                                                                                                                                                                                                                                                       respiratory disorder; cancer; CNS disorder; neurodegenerative disorders;
                                                 1 MARGSLRRLLRLUVLGLWLALLRSVAGEQAPGTAPCSRGSSWSADLDKCMDCA-SC 55
                                                                       MARGSLRRLLRLLVLGLWLALLRSVAGEQAPGTAPCSRGSSWSADLDKCMDCSTSC 56
                                                                                                                                                                                                                                       immunosuppressive; antiinflammatory; antiasthmatic; antiallergic;
Score 274.5; DB 3; Length 112;
Pred. No. 7.2e-21;
1; Mismatches 0; Indels 1
                                                                                                                                                                                                                                                   cytostatic; cerebroprotective; neuroprotective; nootropic; cardiovascular; antiarteriosclerotic; gene therapy; human secreted protein; immune disorder; inflammation;
                                                                                                                                      ADA57390 standard; protein; 112 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                21-MAR-2001; 2001US-0277340P.
19-JUL-2001; 2001US-0306171P.
13-NOV-2001; 2001US-0331287P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                         19-MAR-2002; 2002WO-US008278
 45.1%;
96.4%;
                                                                                                                                                                                                              Human secreted protein #172.
                                                                                                                                                                                     (first entry)
           Similarity 96.4 54; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rosen CA, Ruben SM;
                                                                                                                                                                                                                                                                                                                                                                                         WO2002102994-A2.
                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                  27-DEC-2002.
                                                                                                                                                                                     20-NOV-2003
                                                                                                                                                              ADA57390;
 Query Match
Best Local &
                       Matches
                                                                                                             RESULT 15
                                                                                                                            ADA57390
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                                                                         d
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Job time : 77 secs

New human secreted polypeptides and polymucleotides, useful for diagnosing, treating or preventing e.g. immune disorders, inflammatory conditions, respiratory disorders, cancers, CNS disorders, or neurodegenerative disorders N-PSDB; ADA56496.

2003-167512/16.

Claim 13; SEQ ID NO 1582; 1754pp; English.

neurodegenerative disorders, or polypeptides comprising an amino acid sequence at least 95% identical to the new sequences. The polypeptides, antibodies or antibody fragments that bind to the polypeptides, uncleic acids encoding the polypeptides, agoniers or antagonists that binds to the polypeptide, are useful in preparing diagnostic or pharmaceutical compositions for diagnoshing, treating or preventing an e.g. immune disorders, inflammatory conditions (e.g. inflammatory bowel disease, nephritis or Crohn's disease), respiratory disorders (e.g. asthma and allergy), cancers (e.g. gastric, ovarian or lung cancer), CNS disorders (e.g. multiple sclerosis or ischaemic brain injury), neurodegenerative disorders (e.g. parkinson's disease or Alzheimer's disease), and cardiovascular disorders (e.g. atherosclerosis or myocarditis). The polynucleotides are useful for chromosome identification, chromosome mapping, for controlling gene expression through triple helix formation or antisense DNA or RNA, in gene therapy, for identifying individuals The invention relates to 592 new human secreted polypeptides useful for diagnosing, treating or preventing e.g. immune disorders, inflammatory conditions, respiratory disorders, cancers, CNS disorders, or

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from minute biological samples, in forensic biology, and as hybridization probes. The polypeptides are useful for as molecular weight markers on sodium dedecyl sulfate-polyacrylamide gel electrophoresis (SDS-PAGE) gels, to raise antibodies, for testing biological activities, and for treating or preventing neural disorders, immune system disorders, muscular, reproductive, gastrointestinal, pulmonary, cardiovascular, renal, proliferative and/or cancerous diseases. This sequence corresponds the polypeptide of the invention. Note: The sequence data for this patent did form part of the printed specification, but was obtained ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MARGSLRRLLRLLVLGLWLALLRSVAGEQAPGTAPCSRGSSWSADLDKCMDCA-SC 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MARGSLRRILINILVLGLWLALLRSVAGEQAPGTAPCSRGSSWSADLDKCMDCSTSC
                                                                                                                                                                                                                                                                                                                                                                                                                         1;
                                                                                                                                                                                                                                                                                                                                                              ch 45.1%; Score 274.5; DB 6; Length 112; I Similarity 96.4%; Pred. No. 7.2e-21; 54; Conservative 1; Mismatches 0; Indels 1
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                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                      Sequence 112 AA;
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GenCore	(c) 1993	
	Copyright (c) 1993 - 2004	

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OM protein - protein search,

March 1, 2004, 16:41:53 ; Search time 23 Seconds (without alignments) 255.885 Million cell updates/sec	
16:41:53	
2004,	US-10-062-599-59
ri	062
March	US-10-
	Title:
on:	9
Run on:	Title:

608 1 MARGSLRRLLRLLVLGLWLA......LSGFLVWRRCRRERSSPPPX 114 Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

Total number of hits satisfying chosen parameters:

389414 seqs, 51625971 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

1: /cgn2_6/ptcdata/2/iaa/5A_COMB.pep:*
2: /cgn2_6/ptcdata/2/iaa/5B_COMB.pep:*
3: /cgn2_6/ptcdata/2/iaa/6A_COMB.pep:*
4: /cgn2_6/ptcdata/2/iaa/6B_COMB.pep:*
5: /cgn2_6/ptcdata/2/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptcdata/2/iaa/PCTUS_COMB.pep:* Issued Patents AA: Database:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Seguence 59, Appl	139,		228,	2924				2985	31,	31,	26,						Sequence 2, Appli				Sequence 18195, A			Sequence 20688, A		Sequence 28223, A
SUMMARIES	ID	US-09-690-454-59	US-09-489-847-139	US-09-489-847-284	US-09-489-847-228	US-09-252-991A-29249	US-09-252-991A-26145	US-09-252-991A-20063	US-09-252-991A-31619	US-09-252-991A-29850	US-09-322-409-31	US-09-451-527-31	US-09-322-409-26	US-09-451-527-26	US-09-252-991A-18795	US-09-252-991A-21147	US-09-199-637A-287	US-09-252-991A-21454	US-09-462-136-2	US-08-804-227C-10	US-08-804-198-4	US-09-252-991A-22078	US-09-252-991A-18195	US-09-252-991A-25290	US-09-252-991A-24730	US-09-252-991A-20688	US-09-220-528-104	US-09-252-991A-28223
	DB	4	4	4	4	4	4	4	4	4	4	4	4	4	4	4	4	4	4	~	N	4	4	4	4	4	٣	4
	Query Match Length	114	112	155	156	248	400	631	152	249	250	250	276	276	334	305	187	187	1278	3724	3724	478	402	176	152	153	215	511
o¥÷	Query	99.8	45.1	45.1	45.1	15.9	14.6	14.4	13.7	13.2	12.6	12.6	12.6	12.6	12.3	12.3	12.1	12.1	11.8	11.8	11.8	11.8	11.6	11.4	11.3	11.3	11.3	11.3
	Score	607	274.5	274.5	274.5	96.5	88.5	87.5	83.5	80.5	76.5	76.5	76.5	76.5	75	74.5	73.5	73.5	72	72	72	71.5	70.5	69.5	69	69	69	
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Gaps

1 MARGSLRRILRLUVLGLWLALLKSVAGEQAPGTAPCSRGSSWSADLDKCMDCASCRARPH 60

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Sequence 10884, A	Sequence 37, Appl	Sequence 2, Appli	Sequence 2, Appli	Sequence 17414, A	Seguence 17313, A	Seguence 29996, A	Sequence	Sequence	Seguence	Sequence	Sequence	Sequence 23, Appl	Sequence	Sequence	Sequence 90, Appl	Sequence 77, Appl	Sequence 21707, A
US-09-489-039A-10884	US-08-775-009-37	US-07-964-589-2	PCT-US93-02024-2	US-09-252-991A-17414	US-09-252-991A-17313	US-09-252-991A-29996	US-09-252-991A-29124	US-09-252-991A-31958	US-09-252-991A-22300	US-09-383-586-12	US-09-322-409-23	US-09-451-527-23	US-09-322-409-7	US-09-451-527-7	US-09-413-814-90	US-09-413-814-77	US-09-252-991A-21707
7 4	2	1	5	4	4 4	4 4	4	4	5.4	4 3	8	8 4	4	4 4	9	1 3	2 4
127	20	42	42	13	144	50	28	36	77	17	26	268	29	29	35	361	112
11.3	11.3	11.3	11.3	11.2	11.2	11.2	11.2	11.2	11.2	11.1	11.1	11.1	11.1	11.1	11.1	11.1	11.0
68.5	68.5	68.5	68.5	68	68	68	89	68	68	67.5	67.5	67.5	67.5	67.5	67.5	67.5	67
28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

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        US-09-09-0-424-7

US-09-09-0-424-7

Batent No. 653147

GENERAL INFORMATION:

TITLE OF INVENTION: 32 Human Secreted Proteins

FILE REFERENCE: PZ006P1

CURRENT FILING DATE: 2000-10-18

PRIOR APPLICATION NUMBER: 09/189,144

PRIOR PELICATION NUMBER: 09/189,144

PRIOR PELING DATE: 1998-11-10

PRIOR PELING DATE: 09/04,039

PRIOR PELING DATE: May 30, 1997

PRIOR PELING DATE: May 30, 1997

PRIOR FILING DATE: May 30, 1997

PRIOR FILING DATE: May 30, 1997

PRIOR PELING DATE: May 30, 1997

PRIOR PILING DATE: AUGUSE 29, 1997
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; OTHER INFORMATION: Xaa equals stop translation
US-09-690-454-59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
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US-09-690-454-59
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Best Local S:
Matches 113
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US-09-489-847-228
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SDFCLGCAAAPPAPFRLLWPILGGALSLTFVLGLLSGFLVWRRCRRERSSPPP 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 4; Length 112;
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TITLE OF INVENTION: 98 Human Secreted Proteins
                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/09/489,847

CURRENT FILING DATE: 2000-01-24

EARLIER APPLICATION NUMBER: PCT/US99/17130

EARLIER FILING DATE: 1999-07-29

EARLIER FILING DATE: 1998-07-30

EARLIER FILING DATE: 1998-07-30

EARLIER PILING DATE: 1998-08-05

EARLIER FILING DATE: 1998-08-05

EARLIER FILING DATE: 1998-08-05

EARLIER FILING DATE: 1998-08-05

EARLIER FILING DATE: 1998-08-06

NUMBER OF SEQ ID NOS: 376

NUMBER OF SEQ ID NOS: 376
                                                                                                                                               Sequence 139, Application US/09489847 Patent No. 6476195
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Sequence 29249, Application US/09252991A

Sequence 29249, Application US/09252991A

Patent No. 655195

GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION:
TITLE OF INVENTION:
ABPLICANTON:
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ABPLICANTON:
ABPLICANTON NUMBER: US/09/252,991A

CURRENT APPLICANTON NUMBER: US/09/252,991A

CURRENT FILING DATE: 1999-02-18

FRIOR FILING DATE: 1998-02-18

FRIOR FILING DATE: 1998-02-18

FRIOR FILING DATE: 1998-02-18

FRIOR FILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

LENGTH: 248
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                                                                                                              1 MARGSIRRLIRLIVLGLWLALIRSVAGEQAPGTAPCSRGSSWSADLDKCMDCA-SC 55
                                                                                                                                                        1 MARGSLRRLLRLLVLGLWLALLRSVAGEQAPGTAPCSRGSSWSADLDKCMDCSTSC 56
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H
     Length 155;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
  Score 274.5; DB 4;
Pred. No. 1.3e-22;
1; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: SITE
LOCATION: (156)
OTHER INFORMATION: Xaa equals stop translation
                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Rosen et al
TITLE OF INVENTION: 98 Human Secreted Proteins
FILE REFERENCE: PZ031P1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TIER KETERION NUMBER: US/09/489, 847
CURRENT FILING DATE: 2000-01-24
EARLIER APPLICATION NUMBER: PCT/US99/17130
EARLIER PILING DATE: 1999-07-29
EARLIER PILING DATE: 1998-07-29
EARLIER FILING DATE: 1998-08-05
EARLIER FILING DATE: 1998-08-05
EARLIER FILING DATE: 1998-08-05
EARLIER FILING DATE: 1998-08-05
EARLIER FILING DATE: 1998-08-12
EARLIER PILING DATE: 1998-08-12
EARLIER PILING DATE: 1998-08-06
EARLIER PILING DATE: 1998-08-06
EARLIER FILING DATE: 1998-08-06
EARLIER FILING DATE: 1998-08-06
EARLIER FILING DATE: 1998-08-06
NUMBER: 06/095,455
EARLIER FILING DATE: 1998-08-06
SEQ.ID NOS: 376
SEQ.ID NO 228
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                                                                                                                                                                                                                                                                                                              Sequence 228, Application US/09489847
Patent No. 6476195
GENERAL INFORMATION:
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ORGANISM: Pseudomonas aeruginosa
Query Match
Best Local Similarity 96.4%;
Matches 54; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 96.4
Matches 54; Conservative
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Sequence 29850, Application US/09252991A

Patent No. 6551795
GRNERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: ARRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: ARRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1999-02-18
PRIOR FILING DATE: 1999-02-18
PRIOR FILING DATE: 1999-07-17
NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER: PRIOR PRIOR DATE: 1998-07-27
NUMBER: PRIOR PRIOR DATE: 1998-07-27
                                                                                                                                                                                                                                                                          APPLICANT: MARCA J. Rubenfield et al.
APPLICANT: MARCA J. Rubenfield et al.
TITLE OF INVENTION: NUCLEICA AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US 60/074,788
PRIOR PILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ch 13.7%; Score 83.5; DB 4; Length 152; 1 Similarity 29.7%; Pred. No. 0.11; 30; Conservative 7; Mismatches 37: Indele 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10 LRILVLGLWLALLRSVAGEQAPGTAPCSRGSSWSADLDKCMDCASC-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                75 FRLLWPILGGALSLTFVLGLLSGFLVWRRCRRE---RSSPP 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -----WRRCNRAWGWROSPP 147
112 RSSRKSRVPPAWPCVRGSRDWQCAPWRACCRGSCATCSATP-
                                                                      79 WPILGGALSLTFVLGLLSGFLVWRRCRRERSS 110
                                                                                                                  163 WGRAGVAARYAWRCGTLAGASPPTSCRRSSSS 194
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                                                                                                                                                                                                                              Sequence 31619, Application US/09252991A
Patent No. 6551795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         !: Pseudomonas aeruginosa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            118 APATWSASGGRCAGN-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      40; Conservative
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                                                                                                                                                                                       RESULT 8
US-09-252-991A-31619
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US-09-252-991A-29850
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM
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APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEEC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: NUCLEEC ACID AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 20063, Application US/09252991A

Patent No. 6551795
GENERAL INFORMATION:
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: ARRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US/09/252,991A

CURRENT FILING DATE: 1999-02-18
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                                                                                                                                           --SWSADLDKCM 50
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                                                                                                                                                                                    38 WCSSTRSGGAACRRCCRASSTAPCSRASPSATAAPRIRIGSNCWAGAAPICWSAIISRCR 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18 WLALLRSVAGEOAPGTAPCS--RGSSWSADLDKCMDCASCRARPHSDFCLGCA-AAPPAP
                                                                                                 Gaps
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                                                Length 248;
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Pred. No. 0.091;
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                                                                                            Indels
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                                              5; DB 4; 1
0.007;
ches 23;
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                                                Score 96.5; D
Pred. No. 0.00
9; Mismatches
                                                                                                                                                                                                                                                                                 98 GCASSRARRTGRWCAACSAPVASPPAAWK 127
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                                                                                                                                                                                                                                   51 DCASCRARPHSD-FCLGCA---AAPPAPFR 76
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PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR PELICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 20063
                                                                                                                                           18 WLALLRSVAGE----QAPGTAPCSRGS-
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1 Similarity 38.3%;
23; Conservative 4
                                                15.9%;
30.0%;
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1 Similarity 32.6%;
30; Conservative
                                              Query Match
Best Local Similarity 30.0
Matches 27; Conservative
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Best Local Similarity
Matches 30; Conservat
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Matches 23; Conserv
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US-09-252-991A-26145
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US-09-252-991A-26145
    US-09-252-991A-29249
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SEQ ID NO 26145

Query Match

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TYPE: PRT ORGANISM:

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; ORGANISM: Canis familiaris US-09-451-527-31
                                                                                                                                               Best Local Similarity
Matches 36; Conserv
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Patent No. 6471957;
Facent No. 6471957;
Jerbert Inc. 6471957;
Jerbert In
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       ----PILGGALSLTFVLGLLSGFLV 100
                                                                           160 RPTFSPFRRSRSCQAAASAATPAPSATLWVLVKHRRMAAPI---SLSLT----- 205
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APPLICANT: Sim, Gek-Kee
APPLICANT: Dealtz, Matthew J.
APPLICANT: Dreitz, Matthew J.
APPLICANT: Dreitz, Matthew J.
APPLICANT: Wonderling, Ramani S.
TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC TITLE OF INVENTION: ACID MOLECULES, AND USES THEREOF
FILE REFERENCE: IM-2-C2
CURRENT APPLICATION NUMBER: US/09/451,527
CURRENT APPLICATION NUMBER: US/09/451,409
EARLIER APPLICATION NUMBER: G0/087,306
EARLIER PILING DATE: 1998-05-29
EARLIER PILING DATE: 1998-05-29
NUMBER OF SEQ ID NOS: 174
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; Pred. No. 1.1;
15; Mismatches
           ----HSDFCLGCA-AAPPAPFRLLW-
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Best Local Similarity 27.5%;
Matches 36; Conservative 19
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ORGANISM: Canis familiaris
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LENGTH: 250
TYPE: PRT
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US-09-322-409-31
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                                                                                                                                                                                                                                                                        109 CLELOCOPDSSTLVPPRSPGALEATALPAPOAP-RLILLIL---LPVALLIMSTAWCLHW 164
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Sequence 26, Application US/09451527

Patent No. 6482M103

GENERAL INFORMATION:

APPLICANT: Sim, Gek-Kee

APPLICANT: Pang. Shumin .

APPLICANT: Wonderling, Ramani S.

TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC FILLS OF INVENTION: ACID MOLECULES, AND USES THEREOF

FILE REFERENCE: IM-2-C2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Sim, Gek-Kee
APPLICANT: Yang, Shumin
APPLICANT: Yang, Shumin
APPLICANT: Dreitz, Matthew J.
APPLICANT: Monderling, Ramani S.
TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC
TITLE OF INVENTION: ACAD MOLECULES, AND USES THEREOF
FILE REPERENCE: IM-2-C1
                                                                                                           --EQAPGTAPCSRGSSWSA
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  Length 250;
                                                       Indels
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12.6%; Score 76.5; DB 4; 27.5%; Pred. No. 1.1;
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27.5%; Pred. No. 1.2;
tive 15; Mismatches
                                                          15; Mismatches
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CURRENT FILING DATE: 1999-05-28
EARLIER PEPLICATION NUMBER: 60/087,306
EARLIER FILING DATE: 1998-05-29
NUMBER OF SEQ ID NOS: 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 26, Application US/09322409
Patent No. 6471957
GENERAL INFORMATION:
                                                                                                                 11 RLLVLGLWLALLRSVAG-----
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SEQ ID NO 26
LENGTH: 276
                                                       36; Conservative
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Matches 36; Conservative
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Patent No. 6551795
GENERAL INFORMATION:
PAPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERGIGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REPERENCE: 107136-136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/074,190
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
RIOR APPLICATION NUMBER: US 60/094,190
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 18795
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Pred. No. 2.2;
7; Mismatches 30; Indels
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                                                                                                                                                                                                                                                                                           Score 76.5;
Pred. No. 1.
CURRENT APPLICATION NUMBER: US/09/451,527
CURRENT FILING DATE: 1999-12-01
EARLIER APPLICATION NUMBER: 09/322,409
EARLIER FILING DATE: 1999-05-28
EARLIER FILING DATE: 1998-05-28
EARLIER FILING DATE: 1998-05-29
NUMBER: OF SEQ ID NOS: 174
SOFTWARE: PATENTIN VOIC: 2.0
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GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                           12.6%;
27.5%;
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Best Local Similarity 35.6%;
Matches 26; Conservative
                                                                                                                                                                                                                                                                                                                                                                       11 RLLVLGLWLALLRSVAG-
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                                                                                                                                                                                                                                 ; ORGANISM: Canis familiaris US-09-451-527-26
                                                                                                                                                                                                                                                                                                                                    36; Conservative
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Best Local Similarity
Matches 36; Conserv
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US-09-252-991A-21147
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US-09-252-991A-18795
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                                                                                                                                                                    SEQ ID NO 26
LENGTH: 276
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59 PHSDFCLGCA----AAPPAPFRLLW-----PILGGALSLT-----FVLGLLSGFLVWRR 103
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20 RPSTIRKPAMCSLILWLAESTAAVPSWACSESPETLVMLRSMSWATWLCSSAAVALCWLR
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                      Length 305;
                                                                                                                                                                                                                                                                                                                                                                                                                                       61; Indels
                                                                                                                                                                                                                                                                                                                                                                              ch 12.3%; Score 74.5; DB 4;
1 Similarity 29.1%; Pred. No. 2.3;
37; Conservative 10; Mismatches 61;
                     FILE REFERENCE: 107196.136
CURRENT APPLICATION WUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 21147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Search completed: March 1, 2004, 16:45:09 Job time : 24 secs
                                                                                                                                                                                                                                                                                         ; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-21147
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Best Local Similarity
Matches 37; Conserv
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March 1, 2004, 16:43:58; Search time 33 Seconds (without alignments) 729.439 Million cell updates/sec
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1: \( \text{cgn2} \) \( \text{fordata} \) \( \text{fubbaa} \) \( \text{VBCOMB.ppp:*} \) \( 2 \) \( \text{cgn2} \) \( \text{fordata} \) \( \text{fubbaa} \) \( \text{PUBCOMB.ppp:*} \) \( 2 \) \( \text{cgn2} \) \( \text{fordata} \) \( \text{fubbaa} \) \( \text{PUBCOMB.ppp:*} \) \( 4 \) \( \text{cgn2} \) \( \text{fordata} \) \( \text{fubbaa} \) \( \text{USO} \) \( \text{FMP PUB.ppp:*} \) \( 5 \) \( \text{cgn2} \) \( \text{fordata} \) \( \text{fubbaa} \) \( \text{USO} \) \( \text{PUBCOMB.ppp:*} \) \( 5 \) \( \text{cgn2} \) \( \text{fordata} \) \( \text{fubbaa} \) \( \text{PUBCOMB.ppp:*} \) \( 6 \) \( \text{cgn2} \) \( \text{fordata} \) \( \text{fubbaa} \) \( \text{USOB} \) \( \text{PUBCOMB.ppp:*} \) \( 6 \) \( \text{cgn2} \) \( \text{fordata} \) \( \text{fubbaa} \) \( \text{USOB} \) \( \text{PUBCOMB.ppp:*} \) \( 11 \) \( \text{cgn2} \) \( \text{fordata} \) \( \text{fubbaa} \) \( \text{USOB} \) \( \text{PUBCOMB.ppp:*} \) \( 12 \) \( \text{cgn2} \) \( \text{fordata} \) \( \text{fubbaa} \) \( \text{USOB} \) \( \text{PUBCOMB.ppp:*} \) \( 13 \) \( \text{cgn2} \) \( \text{fordata} \) \( \text{fubbaa} \) \( \text{USOB} \) \( \text{PUBCOMB.ppp:*} \) \( 14 \) \( \text{cgn2} \) \( \text{fordata} \) \( \text{fubbaa} \) \( \text{USOB} \) \( \text{PUBCOMB.ppp:*} \) \( 15 \) \( \text{cgn2} \) \( \text{fordata} \) \( \text{fubbaa} \) \( \text{USOB} \) \( \text{PUBCOMB.ppp:*} \) \( 15 \) \( \text{cgn2} \) \( \text{fordata} \) \( \text{fubbaa} \) \( \text{USOB} \) \( \text{PUBCOMB.ppp:*} \) \( 15 \) \( \text{cgn2} \) \( \text{fordata} \) \( \text{fubbaa} \) \( \text{USOB} \) \( \text{PUBCOMB.ppp:*} \) \( 15 \) \( \text{cgn2} \) \( \text{fordata} \) \( \text{fubbaa} \) \( \text{USOB} \) \( \text{PUBCOMB.ppp:*} \) \( 15 \) \( \text{cgn2} \) \( \text{fordata} \) \( \text{fubbaa} \) \( \text{USOB} \) \( \text{PUBCOMB.ppp:*} \) \( 15 \) \( \text{cgn2} \) \( \text{fubbaa} \) \( \text{USOB} \) \( \text{PUBCOMB.ppp:*} \) \( 15 \) \( \text{cgn2} \) \( \text{fubbaa} \) \( \text{USOB} \) \( \text{PUBCOMB.ppp:*} \) 
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            809742 segs, 211153259 residues
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		Description	Sequence 59, Appl	Sequence 59, Appl	Sequence 4, Appli	Sequence 4, Appli	Sequence 178, App	Sequence 178, App	Sequence 37, Appl	Sequence 444, App	Sequence 1305, Ap	Sequence 5, Appli	Sequence 5, Appli	Sequence 7, Appli	Sequence 7, Appli	Seguence 9, Appli	Sequence 4, Appli
SUMMAKIES		σι	US-10-062-831-59	US-10-062-599-59	US-09-742-454A-4	US-09-883-777-4	US-10-024-298A-178	US-10-042-211A-178	US-10-331-496A-37	US-10-295-027-444	US-10-295-027-1305	US-09-742-454A-5	US-09-883-777-5	US-09-742-454A-7	US-09-883-777-7	US-09-883-777-9	US-10-251-947-4
		DB	14	14	σ	σ	14	14	15	15	15	σ	σ	σ	σ	ወ	14
		Match Length DB	114	114	129	129	129	129	129	129	129	129	129	309	309	300	171
	* 5	Match	99.8	8.66	93.9	93.9	93.9	93.9	93.9	93.9	93.9	74.0	74.0	71.2	71.2	62.4	16.0
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	+[נוספת	No.	H	73	e	4	Ŋ	9	7	80	σ	10	11	12	13	14	15

TYPE: PRT ORGANISM: Homo sapiens

Sequence 7, Appli	Sequence 2, Appli			Sequence 138, App	Sequence 140, App									3127,	3845,	5911,	5912,	64, 7	12,	5165	287,	1189	00	e 5, A	59,	257	Sequence 3192, Ap	Sequence 2, Appli
US-10-251-947-7	-251-947	US-10-251-947-14	US-10-303-685-17	US-10-093-463-138	US-10-093-463-140	US-10-008-063-2	US-10-152-363A-60	US-10-156-761-8962	US-10-218-654-31	US-10-262-439-31	US-10-218-654-26	US-10-262-439-26	US-10-156-761-12251	US-10-108-260A-3127	US-10-108-260A-3845	US-10-369-493-5911	US-10-369-493-5912	US-10-085-198-64	US-10-434-156-12	US-10-369-493-5165	US-09-975-719-287	5-761-11	- 1	US-09-860-836B-5	5	~	US-10-104-047-3192	US-10-208-731-2
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171	170	186	1307	1388	1388	184	184	377	250	250	276	276	732	287	287	635	635	356	548	768	187	409	242	365	365	391	257	1278
16.0	16.0	15.9	14.6	14.6	14.6	14.3	14.3	13.1	12.6	12.6	12.6	12.6	12.6	12.4	12.4	12.4	12.4	12.3	12.2	12.2	12.1	12.1	11.9	11.9	11.9	11.9	11.8	11.8
97.5	97.9	96.5	88.5	88.5	88.5	87	87	79.5	76.5	76.5	76.5	76.5	76.5	75.5	75.5	75.5	75.5	75	74	74	73.5	73.5	72.5	72.5	72.5	72.5	72	72
16	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	4.5

ALIGNMENTS

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GENERAL INCOMATION:

GENERAL INCOMATION:

J TITLE OF INVENTION: 32 Human Secreted Proteins
FILE REFERENCE: PSOOGE1
CURRENT APPLICATION NUMBER: US/10/062,831
CURRENT FILING DATE: 2002-02-05
FRIOR APPLICATION NUMBER: 09/690,454
PRIOR APPLICATION NUMBER: PCT/US98/10868
PRIOR FILING DATE: 1998-11-10
PRIOR APPLICATION NUMBER: PCT/US98/10868
PRIOR FILING DATE: May 30, 1997
PRIOR FILING DATE: AUGUST 29, 1997
Sequence 59, Application US/10062831
Publication No. US20030105297A1
GENERAL INFORMATION:
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1 MARGSERRILRELVEGENTALLERSVAGEQAPGTAPCSRGSSWSADEDECANDCASCRARPH 60
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61 SDFCLGCAAAPPAPFRLLWPILGCALSLTFVLGLLSGFLVWRRCRRERSSPPP 113
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6.3e-48;
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Pred. No. 6.3e-48;
0; Mismatches 6;
                                                                                                                                                                                                                APPLICANT: WILEY, Steven R.
TITLE OF INVENTION: TWEAK Receptor
FILE REFERENCE: 2968-B
FILE REFERENCE: 2968-B
CURRENT APPLICATION NUMBER: US/09/742,454A
CURRENT FILING DATE: 2000-12-19
PRIOR PRIOR APPLICATION NUMBER: 60/172,878
PRIOR FILING DATE: 1999-12-20
PRIOR FILING DATE: 1999-12-20
PRIOR FILING DATE: 2000-05-10
NUMBER OF SEQ ID NOS: 7
SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
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; Sequence 4, Application US/09883777
; Patent No. US20020110853A1
; GENERAL INFORMATION:
    TITLE A. INFORMATION:
    TITLE OF INVENTION: TWEAK RECEPTOR
    FILE REFERENCE: 2968-C
CURRENT APPLICATION NUMBER: US/09/883,777
CURRENT FILING DATE: 2001-06-18
PRIOR APPLICATION NUMBER: US 60/172,878
PRIOR PILING DATE: 1999-12-20
PRIOR PILING DATE: 2000-05-10
PRIOR PILING DATE: 2000-05-10
PRIOR PRILING DATE: 2000-12-19
PRIOR FILING DATE: 2000-12-19
SPRIOR FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 16
; SEQ ID NO 4:
; SEQ ID NO 4:
; SEQ ID NO 4:
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                                                                                                                                  ; Sequence 4, Application US/09742454A; Patent No. US20020041876A1
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Best Local Similarity 94.7%;
Matches 107; Conservative (
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Best Local Similarity 94.77
Matches 107; Conservative
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US-09-883-777-4
                                                                                                                                                                                           GENERAL INFORMATION:
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ORGANISM: Homo
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US-09-883-777-4
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                                                                                                                                                                                                                        0; Indels
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GENERAL INFORMATION:
TITLE OF INVENTION: 32 Human Secreted Proteins
TITLE OF INVENTION: 32 Human Secreted Proteins
TITLE REFERENCE: PZ006P1
CURRENT FILING DATE: 2002-02-05
FRIOR APPLICATION NUMBER: 09/690,454
PRIOR APPLICATION NUMBER: 09/690,454
PRIOR APPLICATION NUMBER: 09/690,454
PRIOR APPLICATION NUMBER: 09/690,454
PRIOR FILING DATE: 1998-11-10
PRIOR FILING DATE: 1998-11-10
PRIOR FILING DATE: MAY 30, 1997
PRIOR PRIOR APPLICATION NUMBER: 60/044,039
PRIOR FILING DATE: MAY 30, 1997
PRIOR FILING DATE: AUGUST 29, 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
99.8%; Score 607; DB 14;
Best Local Similarity 100.0%; Pred. No. 1.8e-51;
Matches 113; Conservative 0; Mismatches 0;
                                                                                                                                                                    99.8%; Score 607; DB 14;
100.0%; Pred. No. 1.8e-51;
tive 0; Mismatches 0;
                            NAME/KEY: SITE

LOCATION: (114)

OTHER INFORMATION: Xaa equals stop translation
US-10-062-0813-59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; OTHER INFORMATION: Xaa equals stop translation US-10-062-599-59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 59
LENGTH: 114
                                                                                                                                                                    Query Match
Best Local Similarity 100.(
Matches 113; Conservative
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US-10-062-599-59
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     FEATURE:
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APPLICANT:
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61 SDFCLGCAAAPPAPFRLLWPILGGALSLTFVLGLLSGFLVWRRCRRERSSPPP 113
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Pred. No. 6.3e-48;
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                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Shuji MURAMATSU
APPLICANT: Vikiko NGGANO
TITLE OF INVENTION: NF-K B Activating Gene
FILE REFERENCE: 1254-0191P
CURRENT APPLICATION NUMBER: 60/314,385
PRIOR APPLICATION NUMBER: 60/314,385
PRIOR FILING DATE: 2001-08-24
PRIOR FILING DATE: 2001-03-26
PRIOR FILING DATE: 2000-12-28
PRIOR FILING DATE: 2000-12-28
PRIOR FILING DATE: 2010-08-24
PRIOR FILING DATE: 2010-08-24
PRIOR FILING DATE: 2010-08-24
PRIOR FILING DATE: 2010-03-26
PRIOR FILING DATE: 2010-03-26
PRIOR FILING DATE: 2001-03-26
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                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: ASAHI KASEI KABUSHIKI KAISHA
                                                                                                                                                                                                                                             Sequence 178, Application US/10024298A Publication No. US20030143540A1 GENERAL INFORMATION:
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SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 178
LENGTH: 129
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Matches 107; Conservative
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; ORGANISM: Homo sapiens
US-10-024-298A-178
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Best Local Similarity
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US-10-024-298A-178
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TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
TITLE OF INVENTION: TREATMENT OF TUMOR
                                                                                                                                                                                                                                                                                                               0;
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                                                                                                                                                                                                                                                     Length 129;
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                                                                                                                                                                                                                                              Score 571; DB 14;
Pred. No. 6.3e-48;
0; Mismatches 6;
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CURRENT APPLICATION NUMBER: US/10/331,496A
CURRENT FILING DATE: 2002-12-30
PRIOR APPLICATION NUMBER: US 60/345,444
PRIOR PILING DATE: 2002-01-02
PRIOR FILING DATE: 2002-01-25
PRIOR FILING DATE: 2002-01-25
PRIOR FILING DATE: 2002-02-25
PRIOR FILING DATE: 2002-03-26
PRIOR FILING DATE: 2002-03-26
PRIOR FILING DATE: 2002-03-26
PRIOR PILING DATE: 2002-03-27
PRIOR PILING DATE: 2002-03-27
PRIOR PILING DATE: 2002-03-21
PRIOR FILING DATE: 2002-03-21
PRIOR FILING DATE: 2002-03-21
PRIOR FILING DATE: 2002-03-21
PRIOR PILING DATE: 2002-03-21
PRIOR APPLICATION NUMBER: US 60/404,809
PRIOR PILING DATE: 2002-08-19
PRIOR PILING DATE: 2002-08-19
PRIOR PILING DATE: 2002-08-19
PRIOR FILING DATE: 2002-08-19
PRIOR FILING DATE: 2002-08-19
PRIOR FILING DATE: 2002-08-19
PRIOR FILING DATE: 2002-08-21
NUMBER OF SEQ ID NOS: 95
SEQ ID NO 37
SEQ ID NO 37
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Best Local Similarity 94.7%;
Matches 107; Conservative
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WILLIAMS, P. MICKEY
WU, THOMAS D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HILLAN, KENNETH J. PHILLIPS, HEIDI S. POLAKIS, PAUL
NUMBER OF SEQ ID NOS: 182
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 178
LENGTH: 129
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                                                                                                                        TYPE: PRT
CORGANISM: Homo sapiens
US-10-042-211A-178
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APPLICANT:
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us-10-062-599-59.rapb

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SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 1305
LENGTH: 129
                                                                              Glynne, Richard
Hevezi, Peter A.
                                                                                                                                             Mack, David H.
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APPLICANT: Gish, Kurt C.
APPLICANT: Gish, Kurt C.
APPLICANT: Glynne, Richard
APPLICANT: Mack, David H.
APPLICANT: Murray, Richard
APPLICANT: Watson, Susan R.
APPLICANT: Bos Blotechnology, Inc.
TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and TITLE OF INVENTION: Methods of Screening for Modulators of Cancer FILE REFERENCE: 018501-012500US
CURRENT APPLICATION NUMBER: US/10/295,027
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61 SDFCLGCAAAPPAPFRLLWPILGGALSLTFVLGLLSGFLVWRRCRERSSPPP 113
                                    61 SDFCLGCAAAPPAPFRLIMPILGGALSLTFVLGLLSGFLVWRRCRREKFTTF 113

    See File Wrapper or PALM.

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PRIOR APPLICATION NUMBER: US 09/663,733
PRIOR FILING DATE: 2000-09-15
PRIOR FILING DATE: 2001-09-15
PRIOR FILING DATE: 2001-11-13
PRIOR FILING DATE: 2001-11-15
PRIOR FILING DATE: 2001-11-15
PRIOR APPLICATION NUMBER: US 60/332,464
PRIOR APPLICATION NUMBER: US 60/332,464
PRIOR FILING DATE: 2001-11-29
PRIOR FILING DATE: 2001-11-29
PRIOR FILING DATE: 2001-11-29
PRIOR FILING DATE: 2001-11-29
PRIOR FILING DATE: 2001-11-4
PRIOR FILING DATE: 2001-12-14
PRIOR FILING DATE: 2002-01-08
PRIOR FILING DATE: 2002-01-0
PRIOR FILING DATE: 2002-01-10
PRIOR FILING DATE: 2002-02-08
PRIOR FILING DATE: 2002-02-08
PRIOR FILING DATE: 2002-02-13
Remaining Prior Application data removed - S\ NUMBER OF SEQ ID NOS: 1386
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Publication No. US20030232350A1
GENERAL INFORMATION:
APPLICANT: Afar, Daniel
                                                                                                                                                                                                              Sequence 444, Application US/10295027 Publication No. US20030232350Al GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                             APPLICANT: Afar, Daniel
APPLICANT: Aziz, Nacasha
APPLICANT: Ginsberg, Wendy M.
APPLICANT: Gish, Kurt C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Homo sapiens
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US-10-295-027-444
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1 MARGSIRRILIRLIVIGIMLALIRSVAGEQAPGTAPCSRGSSWSADLDKCMDCASCRARPH 60
APPLICANT: Macray, Baylan H.
APPLICANT: Matson, Susan R.
APPLICANT: Watson, Susan R.
APPLICANT: Bos Batechonology, Inc.
TITLE OF INVENTION: Methods of Exceening for Modulators of Cancer
TITLE OF INVENTION: Methods of Screening for Modulators of Cancer
CURRENT APPLICATION NUMBER: US 09/663,733
PRIOR PLING DATE: 2002-11-13
PRIOR PLING DATE: 2001-11-13
PRIOR PLING DATE: 2001-11-13
PRIOR FILING DATE: 2001-11-12
PRIOR FILING DATE: 2001-11-29
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PRIOR PLING DATE: 2002-01-08
PRIOR PLING DATE: 2002-02-04
PRIOR PRIOR PLING DATE: 2002-02-04
PRIOR PLING DATE: 2002-02-04
PRIOR PLING DATE: 2002-02-04
PRIOR PRIOR PLING DATE: 2002-02-04
PRIOR PRIOR PLING DATE: 2002-02-04
PRIOR PRIOR PLING DATE: 2002-02-03
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 SDFCLGCAAAPPAPFRLIMPILGGALSLTFVLGLLSGFLVWRRCRRREKFTTP 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Remaining Prior Application data removed - See File Wrapper or PALM NUMBER OF SEQ ID NOS: 1386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 129;
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93.9%; Score 571; DB 15;
Best Local Similarity 94.7%; Pred. No. 6.3e-48;
Matches 107; Conservative 0; Mismatches 6;
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; Sequence 5, Application US/09742454A
; Patent No. US2022041876A1
; GENERAL INFOXZ041876A1
; APPLICANT: WILEY, Steven R.
TITLE OF INVENTYON: TWEAK Receptor
; FILE REFERENCE: 2968-B
; CURRENT APPLICATION NUMBER: US/09/742,454A
; CURRENT APPLICATION NUMBER: 60/172,878
; PRIOR FILING DATE: 1999-12-20
; PRIOR FILING DATE: 2000-05-10
; PRIOR FILING DATE: 2000-05-10
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PATENTIN VET: 2.0
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RESULT 9

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US-09-742-454A-7
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US-09-883-777-7
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          SEQ ID NO 7
LENGTH: 30
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                                                                                              FEATURE
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                                                                                                                                                                                                                                                                             SDFCLGCAAAPPAPFRLLWPILGGALSLTFVLGLLSGFLVWRRCRRERSSPPP 113
                                                                                                                                                                                                                                                                                                     61 SDFCLGCAAAPPAHFRLLWPILGGALSLVLVLALVSSFLVWRRCRRREKFTTP 113
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                                                                                                         Length 129;
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                                                                                                                                                  22; Indels
                                                                                                       Score 450; DB 9;
Pred. No. 3.4e-36;
6; Mismatches 22,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: THEAK RECEPTOR
FILE REFERENCE: 2964-C
CURRENT APPLICATION NUMBER: US/09/883,777
CURRENT APPLICATION NUMBER: US 60/172,878
PRIOR PELLING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: US 60/172,878
PRIOR FILING DATE: 2000-05-10
PRIOR PELLING DATE: 2000-05-10
PRIOR FILING DATE: 2000-05-10
PRIOR FILING DATE: 2000-12-19
PRIOR FILING DATE: 2000-12-19
PRIOR FILING DATE: 2000-12-19
PRIOR FILING DATE: 2000-12-19
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TITLE OF INVENTION: TWEAK Receptor
FILE REFERENCE: 2968-B
CURRENT APPLICATION NUMBER: US/09/742,454A
CURRENT FILING DATE: 2000-12-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: 60/172,878
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: 60/203,347
PRIOR FILING DATE: 2000-05-10
NUMBER OF SEQ ID NOS: 7
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                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 5, Application US/09883777
Patent No. US20020110853A1
GENERAL INFORMATION:
                                                                                                       Query Match
Best Local Similarity 75.2%;
Matches 85; Conservative
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SEQ ID NO 5
LENGTH: 129
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Best Local Similarity
Matches 85; Conserv
LENGTH: 129
TYPE: PRT
ORGANISM: Mus sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; ORGANISM: Mus sp.
US-09-883-777-5
                                                  ; UKGANASH: HAL
US-09-742-454A-5
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                                                                                                                                                                                                                                                                                                                                                                             1 MARGSLRRLIRLIALVLGLWLALIRSVAGEQAPGTAPCSRGSSWSADLDKCMDCASCRARPH
                                                                                                                                                                                                              Query Match 71.2%; Score 433; DB 9; Length 309;
Best Local Similarity 74.1%; Pred. No. 3.7e-34;
Matches 83; Conservative 2; Mismatches 5; Indels 22; Gaps
                                                                                       OTHER INFORMATION: Description of Artificial Sequence: human TWEAK OTHER INFORMATION: receptor fusion protein construct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 SDFCLGCAAAPPAPFRLLWPILGGALSLTFVLGLLSGFLVWRRCRRERSSPP 112
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US-09-883-777-7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 7, Application US/09883777

Patent No. US20020110853A1

GENERAL INFORMATION:
ADPLICANT: Wiley, Steven R.
TITLE OF INVENTION: TWEAK RECEPTOR
FILE REFERENCE: 2968-C
CURRENT APPLICATION NUMBER: US/09/883,777

CURRENT FILING DATE: 2001-06-18

PRIOR PILING DATE: 1999-12-20
PRIOR FILING DATE: 1999-12-20

PRIOR FILING DATE: 2000-05-10

PRIOR PLICATION NUMBER: US 60/203,347

PRIOR FILING DATE: 2000-05-10

PRIOR PLICATION NUMBER: CT/US00/34755

PRIOR FILING DATE: 2000-12-19

PRIOR FILING DATE: 2000-12-19

PRIOR FILING DATE: 2000-12-19

PRIOR FILING DATE: 2000-12-19

NUMBER OF SEQ ID NOS: 16
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Patent No. US20020110853A1
GENERAL INFORMATION:
APPLICANT: WILEY, Steven R.
ITLE OF INVENTION: TWEAK RECEPTOR
FILE REFERENCE: 2968-C
CURRENT APPLICATION WUMBER: US/09/883,777
CURRENT FILING DATE: 2001-06-18
TYPE: PRT
ORGANISM: Artificial Seguence
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ORGANISM: Artificial Sequence
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Best Local Similarity
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APPLICATION NUMBER: US 60/172,878

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                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                            TYPE: PRT

OGGANISM: Artificial Sequence

FRATURE:
OTHER INFORMATION: Human TWEAK receptor fusion protein construct
US-09-883-777-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                               .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 4, Application US/10251947
Publication No: US20030099990A1
Publication No: US20030099990A1
GENERAL INFORMATION:
APPLICANT: HSU, HAILING
TITLE OF INVENTION: TALL-1 Receptor Molecules and Uses Thereof CURRENT APPLICATION NUMBER: US/10/251,947
CURRENT FILING DATE: 2002-09-20
NUMBER OF SEQ ID NOS: 14
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 4
IENGTH: 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16.0%; Score 97.5; DB 14; Length 171; llarity 31.8%; Pred. No. 0.071; Conservative 9; Mismatches 39; Indels 25,
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PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION WNBER: US 60/203,347
PRIOR FILING DATE: 2000-05-10
PRIOR FILING DATE: 2000-12-19
PRIOR FILING DATE: 2000-12-19
PRIOR FILING DATE: 2000-12-19
PRIOR FILING DATE: 2000-12-19
NUMBER OF SEQ ID NOS: 16
SOFTWARE: Patentin version 3.1
LENGTH: 300
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ORGANISM: Homo sapiens
US-10-251-947-4
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Best Local Similarity
Matches 34; Conserva
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US-10-251-947-4
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Search completed: March 1, 2004, 16:49:45 Job time: 47 secs Sequence 60, Appl Sequence 59, Appl Sequence 59, Appl Sequence 59, Appl Sequence 1079, App Sequence 1079, App Sequence 27, App Sequence 27, Appl Sequence 26, Appl Sequence 64, Appl Sequence 64, Appl Sequence 64, Appl Sequence 67, Appl Sequence 64, Appl Sequence 64, Appl Sequence 67, Appl Sequence 67

Sequence 6914, Appsequence 178, App Sequence 178, App Sequence 631, App Sequence 444, App Sequence 1305, App Sequence 37, App

PCT-US98-10868-60
US-018-1184-59
US-10-062-593-59
US-10-062-831-59
US-10-062-831-59
US-10-062-831-59
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US-09-316-633-265
US-09-445-28A-16
US-09-445-28A-16
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US-09-817-77-5
US-09-817-77-7

Sequence 4882, Ap Sequence 178, App Sequence 16, Appl

Sequence 7, Appli Sequence 4883, Ap Sequence 4884, Ap Sequence 1095, Ap Sequence 1095, Ap Sequence 1582, Ap Sequence 139, App Sequence 139, App Sequence 139, Ap Sequence 1883, Ap Sequence 1883, Ap Sequence 508, Ap

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ALIGNMENTS

2, Appli 5, Appli 7, Appli 7, Appli 7, Appli 9, Appli

Sequence Sequence Sequence Sequence

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Sequence 60, Application PC/TUS9810868
GENERAL INFORMATION:
APPLICANT: Human Genome Sciences, Inc., et al.
TITLE OF INVENTION: 32 Human Secreted Proteins
NUMBER OF SEQUENCES: 120
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 1
PCT-US98-10868-60
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(without alignments)
614.752 Million cell updates/sec
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29: /cgn2_6/ptodata/2/paa/US09_COMB.pep:*

20: /cgn2_6/ptodata/2/paa/US09_COMB.pep:*

20: /cgn2_6/ptodata/2/paa/US09_COMB.pep:*

20: /cgn2_6/ptodata/2/paa/US09_COMB.pep:*

21: /cgn2_6/ptodata/2/paa/US00_COMB.pep:*

22: /cgn2_6/ptodata/2/paa/US00_COMB.pep:*

23: /cgn2_6/ptodata/2/paa/US00_COMB.pep:*

24: /cgn2_6/ptodata/2/paa/US00_COMB.pep:*

25: /cgn2_6/ptodata/2/paa/US00_COMB.pep:*

26: /cgn2_6/ptodata/2/paa/US00_COMB.pep:*

27: /cgn2_6/ptodata/2/paa/US00_COMB.pep:*

28: /cgn2_6/ptodata/2/paa/US00_COMB.pep:*

29: /cgn2_6/ptodata/2/paa/US00_COMB.pep:*

20: /cgn2_6/ptodata/2/paa/US00_COMB.pep:*

20: /cgn2_6/ptodata/2/paa/US00_COMB.pep:*

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20: /cgn2_6/ptodata/2/paa/US00_COMB.pep:*

20: /cgn2_6/ptodata/2/paa/US00_COMB.pep:*
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GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                                                                                         protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                              BLOSUM62
Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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                                                                                                                                                                                                                                                       Title:
Perfect score:
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ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
ZIP: 20850
COMPUTER REALBABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2 CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: PCT/US98/10868
FILING DATE: May 27, 1998
CLASSIFICATION: Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. Description

SUMMARIES

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DB

Query Match Length

Score

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Matches 113; Conservative
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NAME/KEY: SITE
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                                                                                                                                                                                                                                                                                                                                                                                                      Length 114;
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8.9e-51;
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OTHER INFORMATION: Xaa equals stop translation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Steven M. Ruben, et al.
FITLE OF INVENTION: 32 Human Secreted Proteins
FILE REFERENCE: P2006F1
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EARLIER APPLICATION NUMBER: PCT/US98/10868
EARLIER FILING DATE: May 28, 1998
EARLIER APPLICATION NUMBER: 60/044,039
EARLIER FILING DATE: May 30, 1997
EARLIER APPLICATION NUMBER: 60/048,093
EARLIER FILING DATE: May 30, 1997
EARLIER APPLICATION NUMBER: 60/048,190
                                                                                                                                                                                                                                                                                                                                                                                                    Score 607;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/09/189,144 CURRENT FILING DATE: 1998-11-10
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EARLIER APPLICATION NUMBER: 60/048,190
EARLIER FILING DATE: MAY 30, 1997
EARLIER APPLICATION NUMBER: 60/048,356
EARLIER APPLICATION NUMBER: 60/056,250
EARLIER FILING DATE: AUGUST 29, 1997
EARLIER FILING DATE: AUGUST 29, 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      29, 1997
60/056,296
29, 1997
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NUMBER OF SEQ ID NOS: 229
SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                   99.8%; Scor.
100.0%; Pre
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTONNEY/AGENT INFORMATION:
NAME: A. Anders Brookes
REGISTRATION UNUMBER: 36,373
REFERENCE/DOCKET NUMBER: PZ006:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8439
INFORMATION FOR SEQ ID NO: 60:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                  114 amino acids
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LENGTH: 114
TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                        TYPE: amino acid TOPOLOGY: linear
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Best Local Similarity
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Best Local Similarity
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GENERAL INFORMATION
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Indels
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100.0%; Pred. No. 8.9e-51;
live 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE REFERENCE: PZ006P1

FILE REFERENCE: PZ006P1

CURRENT APPLICATION NUMBER: US/10/62,599

CURRENT FILING DATE: 2002-02-05

PRIOR APPLICATION NUMBER: 09/690,454

PRIOR FILING DATE: 2000-10-18

PRIOR FILING DATE: 1998-11-10

PRIOR PLILING DATE: 1998-11-10

PRIOR APPLICATION NUMBER: 60/044,039

PRIOR FILING DATE: May 30, 1997

PRIOR FILING DATE: May 30, 1997

PRIOR PLILING DATE: May 30, 1997

PRIOR APPLICATION NUMBER: 60/048,035

PRIOR APPLICATION NUMBER: 60/048,035

PRIOR FILING DATE: May 30, 1997

PRIOR FILING DATE: May 30, 1997

PRIOR APPLICATION NUMBER: 60/048,101

PRIOR FILING DATE: May 30, 1997

PRIOR PRILING DATE: May 30, 1997

PRIOR FILING DATE: ANGUSE 29, 1997

PRIOR PRILING DATE: ANGUSE 29, 1997

PRIOR APPLICATION NUMBER: 60/056,256

PRIOR FILING DATE: ANGUSE 29, 1997

PRIOR APPLICATION NUMBER: 60/056,293

PRIOR PRILING DATE: ANGUSE 29, 1997

PRIOR PRILING DATE: ANGUSE 29, 1997
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; OTHER INFORMATION: Xaa equals stop translation
US-10-062-599-59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Steven M. Ruben, et al.
TITLE OF INVENTION: 32 Human Secreted Proteins
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 59, Application US/10062599 GENERAL INFORMATION:
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Best Local Similarity 100.0
Matches 113; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Steven M. Ruben,
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SOFTWARE: PatentIn Ver.
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ORGANISM: Homo sapiens
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93.9%; Score 571; DB 1; Length 129;
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Best Local Similarity 94.7%;
Matches 107; Conservative
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ORGANISM: Homo sapiens
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ORGANISM: Homo sapiens
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99.8%; Score 607; DB 26; Length 114;
Best Local Similarity 100.0%; Pred. No. 8.9e-51;
Matches 113; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LOCATION: (114)

OTHER INFORMATION: Xaa equals stop translation US-10-062-831-59
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TITLE OF INVESTIGATION Human Secreted Proteins
FILE REFERENCE: PS907PCT
CURRENT APPLICATION NUMBER: DCT/US02/08277
CURRENT PILING DATE: 2002-03-19
PRIOR PRILING DATE: 2001-11-13
PRIOR FILING DATE: 2001-11-13
PRIOR FILING DATE: 2001-07-19
PRIOR PRILING DATE: 2001-07-19
PRIOR FILING DATE: 2001-03-21
NUMBER OF SEQ ID NOS: 1357
SEQ ID NO 745
FILE REFERENCE: PZ006P1
CURRENT APPLICATION NUMBER: US/10/062,831
CURRENT APPLICATION NUMBER: 09/690,454
PRIOR FILING DATE: 2002-02-05
PRIOR FILING DATE: 1998-11-10
PRIOR FILING DATE: MAY 28, 1998
PRIOR FILING DATE: MAY 30, 1997
PRIOR FILING DATE: AUGUST 29, 1997
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; ORGANISM: Homo sapiens
PCT-US02-08277-745
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NAME/KEY: SITE
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1 MARGSLRRILRILVIGLMIAILIRSVAGEQAPGTAFCSRGSSWSADIDKCMDCASCRARPH 60
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                                                                                                                                    1 MARGSLRRILRLIVLGIMIALIRSVAGEQAPGTAPCSRGSSWSADLDKCMDCASCRARPH 60
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Pred. No. 3.3e-47;
0; Mismatches 6; Indels
Query Match 93.9%; Score 571; DB 1; Length 129; Best Local Similarity 94.7%; Pred. No. 3.3e-47; Matches 107; Conservative 0; Mismatches 6; Indels
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TITLE OF INVENTION: Human Secreted Proteins
FILE REPERENCE: PS903PCT
CURRENT APPLICATION NUMBER: PC1/US02/08279
CURRENT FILING DATE: 2002-03-19
PRIOR APPLICATION NUMBER: US 60/331,287
PRIOR FILING DATE: 2001-11-13
PRIOR FILING DATE: 2001-07-19
NUMBER OF SEQ ID NOS: 642
SEQ ID NOS: 642
SEQ ID NOS: 642
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TITLE OF INVENTION: Human Secreted Proteins
FILE REFERENCE: PS902PCT
CURRENT APPLICATION NUMBER: PCT/US02/08278
CURRENT FILING DATE: 2002-03-19
PRIOR APPLICATION NUMBER: US 60/331,287
PRIOR FILING DATE: 2001-11-13
PRIOR PILING DATE: 2001-07-19
PRIOR APPLICATION NUMBER: US 60/306,171
PRIOR APPLICATION NUMBER: US 60/277,340
PRIOR APPLICATION NUMBER: US 60/277,340
PRIOR FILING DATE: 2001-03-21
NUMBER OF SEQ ID NOS: 1988
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 1079
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; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: (1)...(27)
US-09-316-633-265
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Best Local Similarity
Matches 107; Conserv
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; LOCATION: (1)...(27)
US-09-307-140-627
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US-09-316-633-265
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                                                                                                                                                       1 MARGSLRRILIKILUVLGLWLAIIRSVAGEQAPGTAPCSRGSSWSADLDKCMDCASCRARPH 60
                                                                                                 1 MARGSIRRILRILVIGIWIALIRSVAGEQAPGTAPCSRGSSWSADIDKCMDCASCRARPH 60
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   Pred. No. 3.3e-47;
0; Mismatches 6; Indels
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SMITH, VICTORIA
SPENCER, SUSAN D.
WILLIAMS, P. MICKEY
WU, THOMAS D.
94.78;
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APPLICANT: HILLAN,KENNETH J.
APPLICANT: PHILLIPS,HEIDI S.
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Best Local Similarity 94.7
Matches 107; Conservative
                                           107; Conservative
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SEQ ID NO 37
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ORGANISM: Homo sapien
       Best Local Similarity
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PCT-US02-41798A-37
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Sequence 627, Application US/09307140; GENERAL INFORMATION: APPLICANT: Gearing, David P.

US-09-307-140-627

RESULT 9

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APPLICANT: Holtzman, Douglas A.
APPLICANT: Robison, Keith E.
TITLE OF INVENTION: Nucleic Acid Molecules Derived from a TITLE OF INVENTION: Nucleic Acid Molecules Derived from a TITLE OF INVENTION: Human Aortic Endothelium Library FILE REFERENCE: MLN99-14ph
CURRENT APPLICATION NUMBER: US/09/307,140
CURRENT FILING DATE: 1999-05-07
RABLIER APPLICATION NUMBER: 60/084,565
BARLIER FILING DATE: 1998-05-07
NUMBER OF SEQ ID NOS: 1168
SOFTWARE: FASESEQ for Windows Version 3.0
SEQ ID NO 627
LENGTH: 129
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APPLICANT: Holtzman, Douglas A.
APPLICANT: Holtzman, Douglas A.
APPLICANT: Holtzman, Douglas A.
TITLE OF INVENTION: Nucleic Acid Molecules Derived from a TITLE OF INVENTION: Human Mesangial Cell Library
FILE REFERENCE: MIN98-16pA
CURRENT APPLICATION NUMBER: US/09/316,633
CURRENT FILING DATE: 1999-05-21
PRIOR APPLICATION NUMBER: 60/087,052
PRIOR APPLICATION NUMBER: 60/087,052
NUMBER OF SEQ ID NOS: 422
SOFTWARE: PRESEQ for Windows Version 3.0
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Best Local Similarity 94.74
Matches 107, Conservative
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ORGANISM: Homo sapiens
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ORGANISM: Homo sapiens
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Sequence 220, Application US/09465587 GENERAL INFORMATION:
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NUMBER OF SEQ ID NOS: 158
SOFTWARE: PERL Program
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Matches 107; Conservative
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ORGANISM: Homo sapiens
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US-09-465-587-220
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SEQ ID NO 64
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APPLICANT: Kato, Seishi
APPLICANT: Kato, Seishi
APPLICANT: Kato, Seishi
APPLICANT: Kato, Seishi
APPLICANT: Kimura, Tomoko
TITLE OF INVENTION: HUMAN PROTEINS HAVING TRANSMEMBRANE
TITLE OF INVENTION: HUMAN PROTEINS ADDING THESE PROTEINS
FILE REFERENCE: GIN-GFOGEUS
CURRENT FILING DATE: 1999-12-01
PRIOR FILING DATE: 1999-12-01
PRIOR FILING DATE: 1999-06-03
PRIOR FILING DATE: 1998-06-03
PRIOR FILING DATE: 1997-06-03
PRIOR FILING DATE: 1997-06-03
SOFTWARE: FASELSEQ for Windows Version 4.0
SEQ ID NO 16
LEAGTH: 129
                GENERAL INFORMATION:
APPLICANT: Kato, Seishi
APPLICANT: Sekine, Shingo
APPLICANT: Sekine, Shingo
APPLICANT: Sekine, Shingo
APPLICANT: Sekine, Shingo
TITLE OF INVENTION: HUMAN PROTEINS HAVING TRANSMEMBRANE
TITLE OF INVENTION: DOMAINS AND DNAS ENCODING THESE PROTEINS
FILE OF INVENTION: DOMAINS AND DNAS ENCODING THESE PROTEINS
FILE REFERENCE: GIN-6706CPUS
CURRENT APPLICATION NUMBER: US/09/445,258
CURRENT FILING DATE: 1999-12-01
PRIOR FILING DATE: 1999-06-03
PRIOR FILING DATE: 1998-06-03
PRIOR FILING DATE: 1997-06-03
NUMBER OF SEQ ID NOS: 54
SOFTAMER FREE FREEDOM SELECTION NINDERS
SOFTAMER FREEDOM SELECTION 
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Pred. No. 3.3e-47;
0; Mismatches 6; Indels
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94.7%; Pred. No. 3.3e-47;
tive 0; Mismatches 6;
Sequence 16, Application US/09445258
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Best Local Similarity 94.7<sup>1</sup>
Matches 107; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; ORGANISM: Homo sapiens
US-09-445-258-16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
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1 MARGSLRRLLRLLVLGLWIALLRSVAGEQAPGTAPCSRGSSWSADLDKCMDCASCRARPH 60
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APPLICANT: Gearing, David P.
APPLICANT: Gearing, David P.
APPLICANT: Holtzman, Douglas A.
APPLICANT: Robison, Keith E.
TITLE OF INVENTION: NUCLEIC ACID MOLECULES DERIVED FROM A
TITLE OF INVENTION: HUMAN ADULT EPIDERMAL KERATINOCYTE LIBRARY
FILE REPERENCE: 1600.1080-001
CURRENT APPLICATION NUMBER: US/09/465,587
CURRENT APPLICATION NUMBER: 05/114,591
PRIOR APPLICATION NUMBER: 60/114,591
PRIOR PILING DATE: 1999-12-31
NUMBER OF SEQ ID NOS: 356
SOFTWARE: FRAUSEQ for Windows Version 4.0
SEQ ID NO 220
LENGTH: 129
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: HILMMAN, Jennifer L.
APPLICANT: GUEGLER, Karl J.
APPLICANT: COBLEY, Karl J.
APPLICANT: CORLEY, Neil C.
APPLICANT: DANDMAN, Olga
APPLICANT: PATTERSON, Chandra
APPLICANT: GORGONE, Gina A.
APPLICANT: KASER, Matthew R.
APPLICANT: KASER, Matthew R.
APPLICANT: MATCH Nariah R.
APPLICANT: AU-YOUNG, Janice
TITLE OF INVENTION: HUMAN TRANSMEMBRANE PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 571; DB 18;
Pred. No. 3.3e-47;
0; Mismatches 6;
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CURRENT APPLICATION NUMBER: US/09/700,590A
CURRENT FILING DATE: 2001-04-16
PRIOR APPLICATION NUMBER: 60/091,260
PRIOR FILING DATE: 05-29-1998
PRIOR FILING DATE: 07-02-1998
PRIOR PILING DATE: 07-02-1998
PRIOR PELING DATE: 10-02-1998
PRIOR FILING DATE: 10-02-1998
PRIOR FILING DATE: 10-02-1998
PRIOR PLICATION NUMBER: 60/102,954
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us-10-062-599-59.rapm

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1 MARGSLRRILRILVLGLWLALLRSVAGEQAPGTAPCSRGSSWSADLDKCMDCASCRARPH 60
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0
                                                                                                                   Query Match 93.9%; Score 571; DB 21; Length 129; Best Local Similarity 94.7%; Pred. No. 3.3e-47; Matches 107; Conservative 0; Mismatches 6; Indels
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No: 2454048
US-09-700-590A-64
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US-US-142-4544-4 SEQUENCE 4, Application US/09742454A SENERAL INFORMATION:
APPLICANT: WILEY, Seven R.
TITLE OF INVENTION: TWEAK Receptor
FILE REFERENCE: 2968-B
CURRENT APPLICATION NUMBER: US/09/742,454A
CURRENT PILING DATE: 2000-12-19
PRIOR APPLICATION NUMBER: 60/172, 878
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: 60/203,347
PRIOR FILING DATE: 2000-05-10
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PATENTIN VEY: 2.0
SEQ ID NO 4
LENGTH: 129 ; TYPE: PRT; ORGANISM: Homo sapiens US-09-742-454A-4 RESULT 15 US-09-742-454A-4

1 MARGSLRRLLRLLVLGLWLALLRSVAGEQAPGTAPCSRGSSWSADLDKCMDCASCRARPH 60 1 MARGSLRRLLRLLVLGLWLALLRSVAGEQAPGTAPCSRGSSWSADLDKCMDCASCRARPH 60 0; Gaps Query Match
Best Local Similarity 94.7%; Pred. No. 3.3e-47;
Matches 107; Conservative 0; Mismatches 6; Indels δ q

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61 SDFCLGCAAAPPAPFRLLWPILGGALSLTFVLGLLSGFLVWRRCRRERSSPPP 113 SDFCLGCAAAPPAPFRLLWPILGGALSLTFVLGLLSGFLVWRRCRREKFTTP 113

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Search completed: March 1, 2004, 16:48:23 Job time : 182 secs

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Sequence 33810, A Sequence 120, App Sequence 10, Appl Sequence 46659, A Sequence 4, Appl Sequence 11, Appl Sequence 1100, App Sequence 1010, Appl 
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Sequence 60623, A
Sequence 58471, A
Sequence 41647, A
Sequence 33311, A
Sequence 33311, A
Sequence 38237, A
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Sequence 1014, Ap
                                                                                                                                                                       March 1, 2004, 16:43:08 ; Search time 10 Seconds
   (without alignments)
   102.796 Million cell updates/sec
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Sequence 101
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Sequence 8
Sequence 8
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Sequence
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(cgn12_6/ptodata/1/paa/USO5_NEW_COMB.pep:*

(cgn2_6/ptodata/1/paa/USO5_NEW_COMB.pep:*

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(cgn2_6/ptodata/1/paa/USO3_NEW_COMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-10-767-701-33810
US-10-66-762-10
US-10-66-762-10
US-10-767-701-46659
US-10-767-701-46659
US-10-767-701-43640
US-10-767-701-43640
US-10-767-701-43640
US-10-767-701-1010
US-10-767-701-1012
US-10-767-701-1012
US-10-767-701-60623
US-10-767-701-60623
US-10-767-701-60623
US-10-767-701-60623
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US-10-767-701-60623
US-10-767-701-84494
US-10-767-701-341647
US-10-767-701-31811
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US-10-451-467A-76
US-10-767-701-37723
US-10-767-471-910
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99762 seqs, 9017151 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                    OM protein - protein search, using sw model
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length: 2000000000
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                                                                                                                                                                             Run on:
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Sequence 927, App Sequence 934, App	12,	Sequence 12, Appl	Sequence 911, App	Sequence 932, App	Sequence 50873, A	Sequence 58367, P	Sequence 38701, A	Sequence 4242, Ap	Sequence 26, Appl	Sequence 35705, A	Sequence 38374, A	Sequence 2, Appli	Sequence 31947, P	Sequence 46607, P	Sequence 42473, P	Sequence 121, App	Sequence 121, App
US-10-767-471-927 US-10-767-471-934	US-10-646-301A-12	US-10-663-208A-12	US-10-767-471-911	US-10-767-471-932	US-10-767-701-50873	US-10-767-701-58367	US-10-767-701-38701	US-10-417-884A-4242	US-60-542-038-26	US-10-767-701-35705	US-10-767-701-38374	US-10-653-913-2	US-10-767-701-31947	US-10-767-701-46607	US-10-767-701-42473	PCT-US04-02188-121	US-10-764-425-121
99	9	9	9	9	9	9	9	9	7	9	9	9	9	9	9	Н	9
1080	1333	1333	2003	2003	108	181	216	71	359	168	255	1615	113	206	228	987	987
10.3	10.3	10.3	10.3	10.3	10.2	10.2	10.1	10.0	10.0	10.0	10.0	10.0	6.6	9.9	6.6	6.6	6.6
62.5	62.5	62.5	62.5	62.5	62	62	61.5	19	61	60.5	60.5	60.5	9	9	9	9	9
27	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43.	44	45

ALIGNMENTS

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APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
CURRENT APPLICATION NUMBER: US, 10/767, 701
CURRENT FILING DATE: 2004-01-29
SEQ ID NOS: 63128
SEQ ID NOS: 63128
LENGTH: 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23 QAPGLAPAPREPRELILICGGPDGAGCRWATDALAWCCRAPPCRLAP----CPTALPALPG 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   65 ---LGCAAAPPAPFRLLWPILGGALSLTFV-----LGLLS---GFLVWRRCRR 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              79 AGSLASCAAPP-----GSASMTVVSRPATALLLIGGLSSAPGPWAWPRCRR 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13.8%; Score 84; DB 6; Length 152; 29.9%; Pred. No. 0.12; ive 3; Mismatches 25; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION: Clone ID: SORBI-28MAY03-C37651_1.pep
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 290, Application US/10772236
GENERAL INFORMATION:
JAPPLICANT: Rosen et. al.
TITLE OF INVENTION: 89 Human Secreted Proteins
FILE REFERENCE: P8751P1
CURRENT APPLICATION NUMBER: US/10/773,236
CURRENT FILING DATE: 2004-02-09
PRIOR APPLICATION NUMBER: 60/331,085
PRIOR FILING DATE: 2001-08-10
FRIOR APPLICATION NUMBER: 60/325,209
FRIOR APPLICATION NUMBER: F07/US02/25107
PRIOR APPLICATION NUMBER: PCT/US02/25107
PRIOR FILING DATE: 2001-09-28
PRIOR APPLICATION NUMBER: PCT/US02/25107
PRIOR FILING DATE: 2002-08-08
                          Sequence 33810, Application US/10767701; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity 29.9
nes 35; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Sorghum bicolor
US-10-767-701-33810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-10-767-701-33810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-10-773-236-290
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Matches
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Sequence 46659, Application US/10767701
GENERAL INFORMATION:
APPLICANT: Kovalic, David K.
APPLICANT: Kovalic, David K.
APPLICANT: Cao, Yinhua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
FILE REFERENCE: 38-21(53535) B
CURRENT APPLICATION NUMBER: US/10/767,701
CURRENT FILING DATE: 2004-01-29
NUMBER OF SEQ ID NOS: 63128
SEQ ID NO 46659
LENGTH: 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           104 GAAWSTTLKFKVNESYSCRYMLGSNKADIHSDKLFNCTAEEPSTTELLKRILILFSEMYV 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ----APFRLLWPILGGALSLTFVLGLLSGFLVWRRCRRERSSP 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               39 GSSWSADLD-KCMDCASCR-----ARPHSDFCLGCAAAPPAPFRLLWPIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
10.9%; Score 66.5; DB 6; Length 229;
Best Local Similarity 28.7%; Pred. No. 7.7;
Matches 25; Conservative 8; Mismatches 29; Indels 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11.1%; Score 67.5; DB 6; Length 368; 34.4%; Pred. No. 9.6; ive 2; Mismatches 23; Indels 1:
                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: POLYPEPTIDES AND POLYNUCLEOTIDES
TITLE OF INVENTION: POLYPEPTIDES AND POLYNUCLEOTIDES
TITLE OF INVENTION: POLYPEPTIDES AND POLYNUCLEOTIDES
FILE REPERENCE: GP-707758B-C1
CURRENT APPLICATION NUMBER: US/10/667,762
CURRENT FILING DATE: 2003-09-22
PRIOR PAPLICATION NUMBER: US/10/407,386
PRIOR FILING DATE: 2003-04-04
PRIOR PELING DATE: 2003-04-04
PRIOR PELING DATE: 2002-10-21
PRIOR PILING DATE: 2002-04-18
PRIOR PILING DATE: 2002-04-18
PRIOR PILING DATE: 2001-11-19
PRIOR PELING DATE: 2001-11-19
PRIOR PILING DATE: 2001-11-19
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US-10-767-701-46659
                                                                                                                                                                                                                                                           Bernard Emile Joseph Gout
                                                                                                                                                                                                 Philippe Laurent Robert
Stephane Clement Krief
                                                                                                             Steven Ruben
George H. Poste
Michel Louis Souchet
   Steven Michael Foord
                              Han Ngoc Trinh
Alexander Taylor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 11.1
Best Local Similarity 34.4
Matches 21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Sorghum bicolor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   65 LGCAAAPP-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: HOMO SAPIENS
                                                                                       Henry Sarau
                                                                                                                                                                                                                                                                                         Eve Mahe
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US-10-767-701-46659
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APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids US-10-773-236-290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LOCATION: (55) OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           31 PGTAPCSRG--SSWSAD---LDKCMDC--ASCRARPHSDFCLG------CAAAP 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         40 PGSWSCSPSILGSWCXTEGILIRCLQAAVATCPRCPTSDILLGGRAVSSWQRTLLCCPGP 99
PRIOR APPLICATION NUMBER: 60/330,629
PRIOR FILING DARE: 2001-10-26
PRIOR PILING DARE: 2002-10-24
PRIOR PLING DARE: 2002-10-24
PRIOR PLING DARE: 2001-11-05
PRIOR PLING DARE: 2001-11-06
PRIOR PLING DARE: 2001-11-06
PRIOR PLING DARE: 2002-21-06
PRIOR PLING DARE: 2002-02-22
PRIOR PLING DARE: 2003-02-22
PRIOR PLING DARE: 2003-02-22
PRIOR PLING DARE: 2003-02-22
PRIOR PLING DARE: 2003-02-22
PRIOR PLING DARE: 2003-02-25
PRIOR PLING DARE: 2003-02-25
PRIOR PLING DARE: 3003-02-25
PRIOR PLING DARE: 3003-02-25
PRIOR PRIOR APPLICATION NUMBER: 60/358,714
PRIOR PLING DARE: 3003-02-25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ganesh M. Sathe
Joyce Yue Mac
Wendy S. Halsey
Jon Chambers
Alison Isobel Muir
Philip Graham Szekeres
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 10, Application US/10667762
GENERAL INFORMATION:
APPLICANT: Erding Hu
APPLICANT: Yuan Zhu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Catherine E. Ellis
Manhanandeeshwar Gattu
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Randall Forrest Smith
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Derk J. Bergsma
Nabil A. Elshourbagy
David Michalovich
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     John W. Quillen, Jr. Erin M. Toland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pamela A. Lane
Menelas N. Pangalos
Melanie Robbins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      |: || | || || 110
100 SXASRVTWP-LAGAL 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              72 PAPFRLLWPILGGAL 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        24; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Usman Shabon
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: SITE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 3
US-10-667-762-10
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APPLICANT:
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APPLICANT:
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APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: RHEUMATOID ARTHRITIS, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CLOOLSOS
CURRENT APPLICATION NUMBER: US/10/767,471
CURRENT PILLING DATE: 2004-01-30
NUMBER OF SEQ ID NOS: 5023
SOFTWARE: FREESEQ for Windows Version 4.0
                                                                                                                                                                                                                                                            and Other Molecules Associated With
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -----GGFGLP 1132
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30 APGIAPCSRG----SSWSADLDKCMDCA-----SCRARPHSDFCLGCAAAPPAFF--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    36 CSRGSSWSADLDKCMDCASCRARPHSDFCLGC----AAAPPAPFRLLWPILGGALSLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                    GENERAL INFORMATION:
APPLICANT: Kovalic, David K.
APPLICANT: Kovalic, David K.
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associal
TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
TITLE PEPERENCE: 38-21(53535) B.
CURRENT APPLICATION NUMBER: US/10/767,701
CURRENT FILING DATE: 2004 01-29
NUMBER OF SEQ ID NOS: 63128
SEQ ID NO 43640
LIENGTH: 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        32;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 189;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 65; DB 6; Length 189
Pred. No. 9;
5; Mismatches 35; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          82 AAPGAVRVSACALPRDLPPLAGGARPA--ALPSLCKLRVWRR 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1088 CLYGEAWG-----MDCALCPAODSDDFEALCNVLRPPAYSPPRP-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ) OTHER INFORMATION: Clone ID: SORBI-28MAY03-C81491_1.pep
US-10-767-701-43640
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10.6%; Score 64.5; DB 6; 29.7%; Pred. No. 65;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   , OTHER INFORMATION: Xaa = Any Amino Acid US-10-767-471-1010
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Sequence 1010, Application US/10767471; GENERAL INFORMATION:
                              99 LEEPLLFNFSMMHCGLLTPACR 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10.7%;
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Best Local Similarity 29.7
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 29.4
Matches 30; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Sorghum bicolor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1133 YEYG 1136
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46 LDK--
                                                                                                                               US-10-767-701-43640
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US-10-767-471-1010
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LENGTH: 1417
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TITLE OF INVENTION: METHOD AND REAGENTS FOR EPITHELIAL BARRIER FORMATION AND
TITLE OF INVENTION: TREATMENT OF MALIGNANT AND BENIGN SKIN DISORDERS BY MODULATING
TITLE OF INVENTION: THE NOTCH PATHWAY
FILE REFERENCE: 22507
CURRENT APPLICATION NUMBER: US/10/762,603
CURRENT FILING DATE: 2004-01-22
PRIOR PELICATION NUMBER: US 60/229,614
PRIOR FILING DATE: 2000-08-31
PRIOR FILING DATE: 2000-08-31
PRIOR FILING DATE: 2001-08-31
NUMBER: OF SEQ ID NOS: 18
SOFTWARE: PALCHAIN VERSION 3.2
SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                65 DECDIYVRVCLKEYQAKVIPIGPCSYGHGAIPVLGGNSFYLPPAGAAGDRARARARAGGD 124
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 6; Length 1238,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                35; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3 RGSLRRLLRLLVLGLW------LALLRSVAGEQAPG---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 11, Application US/10417375A
GENERAL INFORMATION:
APPLICANT: David W. Morris
APPLICANT: Marc Malandar TITLE OF INVENTION: Novel Therapeutic Targets in Cancer FILE REFERENCE: 52945201600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13 LVLGLWLALLRSVAGE-------QAPG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/10/417,375A CURRENT FILING DATE: 2003-04-15
                                                   | :: |||:|| :: 164 SEDFSSERMLGYVAAGVVLGMLSSMFI 190
                       ----GGALSLTFVLGLLSGFLV 100
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SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 66;
Pred. No.
                                                                                                                                                                           Sequence 4, Application US/10762603
GENERAL INFORMATION:
APPLICANT: Nickoloff, Brian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  125 ODPGLVV---IPFOFAWP 139
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Best Local Similarity 26.8
Matches 22; Conservative
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Best Local Similarity 24.6
Matches 34; Conservative
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ORGANISM: Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 6
US-10-417-375A-11
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LENGTH: 271
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US-10-762-603-4
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GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: RHEUMATOID ARTHRITIS, METHODS OF DETECTION AND USES THEREOF
FILE REPRENCE: CL001505
CURRENT APPLICATION NUMBER: US/10/767,471
CURRENT FILING DATE: 2004-01-30
NUMBER OF SEQ ID NOS: 50231
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1013
LENGTH: 1587
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                                                                                                                                                                                                                                                                                                                       1310 CLYGEAWG------MCALCPAQDSDDFEALCNVLRPPAYSPPRP-------GGFGLP 1354
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                                                                                                                                                                                             DB 6; Length 1557;
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GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENERIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: GENERIC POLYMORPHISM, METHODS OF DETECTIV:
FILE REFERENCE: CLO01505
CURRENT APPLICATION NUMBER: US/10/767,471
CURRENT PILLING DATE: 2004-01-30
NUMBER OF SEQ ID NOS: 50231

SOUTHARD: PASILSEQ for Windows Version 4.0

SEQ ID NO 1015
LENGTH: 1587
                                                                                                                                                                                                                                              20; Indels
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Pred. No. 72;
4; Mismatches
                                                                                                                                                                                                Score 64.5; I
Pred. No. 70;
                                                                                                                                                                                                                                                                                       36 CSRGSSWSADLDKCMDCASCRARPHSDFCLGC
NUMBER OF SEQ ID NOS: 50231
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1014
LENGTH: 1557
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Best Local Similarity 29.7%;
Matches 19; Conservative
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Best Local Similarity 29.7%;
Matches 19; Conservative
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Best Local Similarity 29.7%;
Matches 19; Conservative
                                                                                          TYPE: PRT
CRGANISM: Homo sapiens
US-10-767-471-1014
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CORGANISM: Homo sapiens
US-10-767-471-1015
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ORGANISM: Homo sapiens
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US-10-767-471-1013
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US-10-767-471-1015
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                                                               Sequence 1009, Application US/10767471
GRNERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENERIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: RHEUMATOID ARTHRITIS, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CLO01505
FILE REFERENCE: CLO01505
CURRENT APPLICATION NUMBER: US/10/767,471
CURRENT APPLICATION NOWBER: US/10/767,471
SOFTWARE FASESO FOR WINDOWS VERSION 4.0
SEQ ID NO 1009
LENGTH: 1421
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GENERAL INFORMATION:
APPLICANT: CANGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: RHEUMATOID ARTHRITIS, METHODS OF DETECTION AND USES THEREOF
FILE REPERBENGE. CLOUS.OS
CURRENT APPLICATION UNMBER: US/10/767,471
CURRENT FILING DATE: 2004-01-30
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TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: RHEUMATOID ARTHRITIS, METHODS OF DETI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ---MDCALCPAQDSDDFEALCNVLRPPAYSPPRP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TILLE OF INVENTION: RHEUMATOID ARTHRITIS,
FILE REFERENCE: CLOOISOS
CURRENT APPLICATION NUMBER: US/10/767,471
CURRENT FILING DATE: 2004-01-30
SOFTWARE: PASESEQ for Windows Version 4.0
SEQ ID NO. 1011
FERVIEW.
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Best Local Similarity 29.7
Matches 19; Conservative
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ORGANISM: Homo sapiens
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ORGANISM: Homo sapiens
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Best Local Similarity
Matches 19; Conserv
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1355 YEYG 1358
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1219 YEYG 1222
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                          RESULT 9
US-10-767-471-1009
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GENERAL INFORMATION:
APPLICANT: Brissoan, Marie-Clotilde
APPLICANT: Brissoan, Jean-Michel
APPLICANT: Briere, Francine
TITLE OF INVENTION: Compositions and Methods
TITLE OF INVENTION: Compositions and Methods
FILE REFREENCE: Spoil 190
CURRENT APPLICATION NUMBER: US/10/333,177
CURRENT FILING DATE: 2003-01-16
PRIOR APPLICATION NUMBER: EP 00306087.8
PRIOR APPLICATION NUMBER: EP 00306087.8
NUMBER OF SEQ ID NOS: 12
SOFTWARE: Patentin version 3.1
                                                                                                                                                                                                                                                                                                                                                 APPLICANT: CARGILL, Michele et al.

APPLICANT: CARGILL, Michele et al.

TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH

TITLE OF INVENTION: RHEUMATOID ARTHRITIS, METHODS OF DETECTION AND USES THEREOF

FILE REPERENCE: CLOGISOS

CURRENT APPLICATION NUMBER: US/10/767,471

NUMBER OF SEQ ID NOS: 50231

SOFTWARE: FastSEQ for Windows Version 4.0
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                     36 CSRGSSWSADLDKCMDCASCRARPHSDFCLGC-----AAAPPAPFRLLWPILGGALSLT 89
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LOCATION: (1)...(1664)
COTHER INFORMATION: Xaa = Any Amino Acid
US-10-767-471-1012
                                                                                                                                                                                                                                                                                                   Sequence 1012, Application US/10767471 GENERAL INFORMATION: APPLICANT: CARGILL, Michele et al.
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ORGANISM: Homo sapiens
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ORGANISM: Homo sapiens
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Best Local Similarity
Matches 19; Conserv
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NAME/KEY: VARIANT
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LENGTH: 1664
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LENGTH: 115
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 protein search, using sw model OM protein March 1, 2004, 16:40:59; Search time 21 Seconds (without alignments) 522.183 Million cell updates/sec Run on:

1 MARGSLRRLLRLLVLGLWLA......LSGFLVWRRCRRERSSPPPX 114 US-10-062-599-59 608 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283366 Total number of hits satisfying chosen parameters:

283366 segs, 96191526 residues

Searched:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	probable chitinase	probable export pr	biosyr	hypothetical prote	_	_			ribonuclease (EC 3	conserved hypothet	fibrillin-1 precur	probable transcrip	probable amino aci	qlypican precursor	probable beta-lact	hypothetical prote	Fas antigen precur	conserved hypothet	osmoregulated prol	hypothetical prote	probable protein k	diheme cytochrome	glycoprotein precu	receptor-type prot	bone marrow stroma	oligopeptide trans	receptor-like tyro	receptor tyrosine	receptor-like tyro
	QI	T04484	878698	AD0753	B70939	T20910	B87353	T22758	660695	T04420	D75303	A55624	T36798	E95850	I56545	D75330	C70893	JC2395	B69092	E75138	B61213	T00872	T46966	GNVUUK	I50615	JC4390	AH3572	\$51603	S47489	851604
	DB	2	~	ď	~	~	2	~	~	7	~	7	7														7	~	~	~
	Length	332	245	245	436	635	519	768	261	227	346	2871	175	467	558	424	587	324	431	484	480	683	384	1008	1013	319	332	893	9	981
* Query	Match	12.9	12.6	12.6	12.4	12.4	12.3	12.2	12.1	12.0	11.9	11.8	11.7	•	11.5	11.4	11.4	11.3	11.3	11.3	11.2	11.2	11.1	11.1	11.1	11.0	11.0	11.0	11.0	11.0
	Score	78.5	76.5	76.5	75.5	75.5	74.5	74	73.5	73	72.5	72	71	70.5	.70	69.5	69.5	69	68.5	68.5	68	68	67.5	67.5	67.5	63	67	67	67	29
Result	No.	ч	7	e	4	S	9	7	œ	σ	10	77	12	13	14	15	16	17	18	19	20	21	22.	23	24	25			28	29

receptor tyrosine	probable MFS trans	hypothetical prote	conserved hypothet	structural polypro	reverse transcript	trophozoite cystei	notch 3 protein -	hypothetical prote	probable export pr	flagellar biosynth	flagellar biosynth	hypothetical prote	serine/threonine-s	notch3 protein - h	conserved hypothet
S49015	C82987	C36942	E83085	GNWVR3	T07965	A42125	S45306	T49381	B36869	G90964	G85812	F83545	T02731	S78549	F82989
~	~	N	~	-1	N	N	~	7	N	7	C3	7	7	~	~
1005	389	394	549	992	1053	1766	2318	214	245	245	245	206	884	2321	196
17.0	10.9	10.9	10.9	10.9	10.9	10.9	10.9	10.8	10.8	10.8	10.8	10.8	10.8	10.8	10.7
_						9	99	'n	'n	'n	Ŋ	Ŋ	Ŋ	'n	ហ
67 1	66.5	99	99	99	99	φ	ø	65	65	65	65.5	65.	65.	65.5	9

ALIGNMENTS

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Probable chitinase (EC 3.2.1.14) - barley
C'Species: Hordeum vulgare (barley)
C'Accession: T04484
R'Leah, R.; Skriver, K.; Knudsen, S.; Ruud-Hansen, J.; Raikhel, N.V.; Mundy, J.
Plant J. 6, 579-589, 1994
A;Title: Identification of an enhancer/silencer sequence directing the aleurone-specific A;Reference number: 215373; MUID:95079849; PMID:987416
A;Reference number: 215373; MUID:95079849; PMID:7987416
A;Reference number: 215373; MUID:95078849; PMID:7987416
A;Reference number: 215373; MUID:95078849; PMID:7987416
A;Reference number: 215373
A;Referen
```

7; 13 LVLGLWLALLRSV----AGEQAPG-TAP----CSRGSSWSADLDKCMDCASCRARPHSDF 63 Gaps 23; Query Match
Best Local Similarity 32.0%; Pred. No. 3.5;
Matches 33; Conservative 9; Mismatches 38; Indels 2: ð

13 IVLSAALAMAMVVRAQQCGSQAGGATCPNCLCCSRFGYCGSTSDYC--GAGCQSQ CLGCAAAPPAPFRLLWPILGGALSLTFVLGLLSGFLVWR-RCR 105 99 셤 ð g

65

RESULT 2

S78698
probable export protein flip precursor - Salmonella typhimurium
C;Species: Salmonella typhimurium
C;Species: Ol-Feb-1999 #sequence_revision 01-Feb-1999 #text_change 21-Jul-2000

C,Accession: S78698
R;Ohnishi, K.; Fan, F.; Schoenhals, G.J.; Kihara, M.; Macnab, R.M.
Lacteriol. 179, 6092-6099, 1997
A;Title: The FliO, FliP, FliQ, and FliR proteins of Salmonella typhimurium: putative comp. A;Reference number: S78696; MUID:97464436; PMID:9324257
A;Accession: S78698

A; Molecule type: DNA

A;Residues: 1-245 <pus A;Residues: 1-245 <pus A;Cross-references: EMBL:L49021; NID:g1066860; PIDN:AABB1319.1; PID:g1066863
A;Note: the sequence of residues 42-241 and the corresponding nucleic acid sequence are I C;Genetics: A;Gene: flip
A;Gene: flip

us-10-062-599-59.rpr

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S)

Gaps

49;

201

84

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à DP

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A,Accession: B70939
A,Staus: preliminary; nucleic acid sequence not shown; translation not shown
A,Molecule type: DNA
A,Molecule type: DNA
A,Residues: 1-436 <COL>
A,Residues: 1-436 <COL>
A,Cross-references: GB:AL021929; GB:AL123456; NID:g3242291; PIDN:CAA17338.1; PID:e125244;
A,Experimental source: strain H37Rv
A,Experimental source: strain H37Rv
A,Genetics:
A,Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Experimental source: clone F14F7
R; Gardner, A.
submitted to the EMBL Data Library, November 1996
A; Reference number: Z20398
A; Accession: T27646
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: DNA
A; Molecule type: DNA
A; Residues: 1-635
A; Cross-references: EMBL: Z82083; PIDN: CAB04975.1; GSPDB: GN00021; CESP: ZK1010.9
A; Experimental source: clone ZK1010
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   92 PITAYKNGGISF---LIAYVVCGILFAVPAIHMEFALGQYAAKSPPAAFRRMMPILBGVG 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PIDN:CAB04115.1; GSPDB:GN00021; CESP:ZK1010.9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     202 ALPHR--IVPRVHAAPGLHKLVYVGWTAIRTNGWYRRYLLVQVLFGSVVLGSSFHSIRVA 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           hypothetical protein ZK1010.9 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Table: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 21-Jan-2000
C;Accession: T20910; T27646
R;McMurray, A.
submitted to the EMBL Data Library, November 1996
A;Reference number: Z19345
A;Reference number: Z19345
A;Accession: T20910
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-635 <WILL
A;Residues: 1-635 <WILL
A;Cross-references: EMBL;Z81503; PIDN:CAB04115.1; GSPDB:GN00021; CESP:ZKL010
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                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MARGSLRRLLRLLVLGLWLALLRSVAGEQA--PGTAPCSRGSS--WSADLDKCMDCASCR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         142 MPSGTARARILLITEVGVGAALTAVVAATLSFVPDQHPLSRNIHLLWTAAVAMAISAAICR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ----PIIGG---
                                                                                                                                                                                                                                                                                                  12.4%; Score 75.5; DB 2; Length 436; 23.0%; Pred. No. 8.4; ive 16; Mismatches 52; Indels 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 635;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            28; Indels
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A;Introns: 71/3; 184/2; 316/3; 403/1; 444/3; 547/3; 577/3
C;Superfamily: gamma-aminobutyric acid transporter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12.4%; Score 75.5; DB 2; 36.6%; Pred. No. 11; tive 10; Mismatches 28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ---ALSLTFVLGLLSGFLVWRRCR 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 260 AVPGDQPDEVVAVVLFVCVGLLGGIALWNRVR 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                57 ARPHSDFCLGCAAAPPAPFRLLW--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity 36.6
nes 26; Conservative
                                                                                                                                                                                                                                                                                                                                                                         35; Conservative
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                                                                                                                                                                                                                                                                                                                                      Similarity
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                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      flagellar biosynthetic protein Flip [imported] - Salmonella enterica subsp. enterica ser C;Species: Salmonella enterica subsp. enterica servoar Typhi A;Note: this species has also been called Bindonella typhi C;Date: this species has also been called Solmonella typhi C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999
C;Accession: B70939
S; Conor, R.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S; Conor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S. Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Mature 33, 537-544, 1998
A) Authors: Sqares, R.; Sulson, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A; Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome A; Reference number: A70500; MUID: 98295987; PMID: 9634230
   C;Function:
A;Description: may be involved in flagellar assembly; may be involved in export of flage C;Superfamily: flagellar biosynthetic protein flip C;Superfamily: flagellum; transmenbrane protein C;Keywords: flagellum; transmenbrane protein c;Keywords: flagellum; transmenbrane mradiched <STG>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Accession: AD0753
R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, H. T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; A;Hill: Complete genome sequence of a multiple drug resistant Salmonella enterica serov A;Reference number: AB0502; MUID:21534947; PMID:11677608
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9
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A;Residues: 1-245 <PAR>
A;Cross-references: GB:AL513382; PIDN:CAD05727.1; PID:g16503220; GSPDB:GN00176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6 LRRLLRLLVLGLWLALLRSVAGEQAPG--TAP-CSRGSSWSADLDKCMDCASCRARP--- 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 HRELFLSLAGEW--LFSPAAAAQLPGLISQPLAGGGGSWSLSVQTLVFITSLTFLPAIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6 LRRILIRLLVLGLWLALLRSVAGEQAPG--TAP-CSRGSSWSADLDKCMDCASCRARP---
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                                                                                                                               Fil-21/Domain: signal, sequence #status predicted <SIG>Fi2-245/Product: probable export protein flip #status predicted <MAT>Fi2-2-245/Product: probable export protein flip #status predicted <MAT>Fi9-561/Domain: transmembrane #status predicted <TM2>Fi89-105/Domain: transmembrane #status predicted <TM2>Fi189-205/Domain: transmembrane #status predicted <TM3>Fi18-228/Domain: transmembrane #status predicted <TM3>Fi18-228/Domain: transmembrane #status predicted <TM4>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             27;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              59 LAMISFIRIIVFGLLRNALGTPSAPPNQV----LLGLALFLTFFI 100
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                                                                                                                                                                                                                                                                                                                                                                             12.6%; Score 76.5; DB 2; Length 245; 30.8%; Pred. No. 4.3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -----CLGCAAAPPAPFRLLWPILGGALSLTFVL 92
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLGCAAAPPAPFRLLWPILGGALSLTFVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                38;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Gene: STY2187
C;Superfamily: flagellar biosynthetic protein flip
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No. 4.3; 9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                9; Mismatches
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Pred. No. 4.
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1 Similarity 30.8%;
33; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                33; Conservative
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Best Local Similarity
Matches 33; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AyStatus: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       60 --HSDF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Accession: AD0753
                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
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Gaps

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A,Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: functi A,Reference number: A69000, MUID: 98037514; PMID: 9371463
A,Accession G69099
A,Status: preliminary; nucleic acid sequence not shown; translation not shown A,Status: DNA
A,Residues: 1.261 AMTH>
A,Residues: 1.261 AMTH>
A,CCOBS-references: GB.AB000929; GB.AB000666; NID: 92622853; PIDN: AAB86210.1; PID: 92622871
A,Experimental source: strain Delta H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conserved hypothetical protein - Deinococcus radiodurans (strain R1)
C;Species: Deinococcus radiodurans
C;Species: Deinococcus radiodurans
C;Species: Dec-1999 #sequence_revision 03-Dec-1999 #text_change 17-Mar-2000
C;Accession: D75303
R;White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.; F., M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Maj. Sinith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
A;Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
A;Reference number: A75250; MUID:20036896; PMID:10567266
A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Residues: 1-227 <ROG>
A;Cross-references: EMBL:AF000940; NID:g2150001; PIDN:AAB58719.1; PID:g2150002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -RPHS---DFCLGCA-AAPPA 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21 LLRSVAGEQAPGTAPCSRG-SSWSADLDKCMDCASCRARPHSDFCLGCAAAPPAPFRLLW 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ribonuclease (EC 3.1.-.-) - barley
C;Species: Hordeum vulgare (barley)
C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 22-Jun-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14;
                                                                                                                                                                                                                                                                                                                                                                                                                      12.1%; Score 73.5; DB 2; Length 261; 29.2%; Pred. No. 8.8; tive 8; Mismatches 21; Indels 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ch 12.0%; Score 73; DB 2; Length 227; I Similarity 30.0%; Pred. No. 8.8; 30; Conservative 11; Mismatches 45; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          80 PIL-----GGALSLTFVLGLL---SGFLVWRRCRRERS 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    148 ALASAGVAPDGGYYTLSAVKGAIQQGTGFEPFVECNRDES 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             31 PGTAPCSRGSSWSA-----DLDKCMDCASCRA--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Accession: T04420
R;Rogers, J.C.; Rogers, S.W.
submitted to the EMBL Data Library, April 1997
A;Accession: T04420
                                                                                                                                                                                                                                                                                                                              C;Superfamily: pyruvate synthase gamma chain C;Keywords: coenzyme A; oxidoreductase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C; Superfamily: Enterobacter ribonuclease C; Keywords: hydrolase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Experimental source: cv. Igri
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 29.2
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 30; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   | : :
251 PVKAI 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           74 PFRLL 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Introns: 35/3; 87/3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: DNA
                                                                                                                                                                                                                                                                                               A;Gene: MTH1740
                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          à
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C; Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 20-Apr-2001
C; Accession: BB7353
R; Mierman, W.C.; Feldblyum, T.V.; Paulsen, T.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J. B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon n. J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M. A; Title: Complete Genome Sequence of Caulobacter crescentus.
A; Reference number: A87249; MUID:21173698; PMID:11259647
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             probable pyruvate synthase (EC 1.2.7.1) gamma chain - Methanobacterium thermoautotrophid (Species: Methanobacterium thermoautotrophicum (Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 05-May-2000 (Spacession: 669099 R;Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.; Qiu, D.; Spadafora, R.; Vicainire, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiwani, N. ki, S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N. J. Bacteriol. 179, 7135-7155, 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-768 <WILL
A;Coss-references: EMBL: 281091; PIDN: CAB03142.1; GSPDB:GN00019; CESP:F55H12.1
A;Experimental source: clone F55H12
                                                                                                                                                                                                                                                                                                                                                            A;Residues: 1-519 <STO>
A;Cross-references: GB:AE005673; NID:g13422090; PIDN:AAK22822.1; GSPDB:GN00148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     52 CASCRARPHSDFCLGCAAAPPAPFRLL------WPILGGALSLTFVLGLLSGFLVWRR 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            --SWSADLDKCMD 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            hypothetical protein F55H12.1 - Caenorhabditis elegans
C;Species: caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 17-Mar-2000
C;Accession: T22758
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               31; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Map position: 1
A;Introns: 114/3; 189/1; 301/2; 426/3; 513/1; 554/3; 657/3; 687/3; 741/1
C;Superfamily: gamma-aminobutyric acid transporter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CAFVFAVPAIHMEFALGQYAAKSPPAVFRRIMPALEGVGWMTCIVGAVIG 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 2; Length 519;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 768;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9 LIRLLVLGLWLALLRS-VAGEOAPGTAPCSRGS--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ribobson, R. submitted to the EMBL Data Library, October 1996 A; Reference number: 219610 A; Recession: T22758
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12.3%; Score 74.5; I
24.3%; Pred. No. 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 74; DB
Pred. No. 18;
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CRRERS-----SPPP 113 370 VSAEDTPDLLAISPTP 385

104

Best Local Similarity 24.39 Matches 33; Conservative

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A; Gene: CC0837 Query Match

C; Genetics:

A; Accession: B87353 A; Status: preliminary A; Molecule type: DNA

12.2%;

Query Match Best Local Similarity

A; Gene: CESP:F55H12.1

20; Conservative

153

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Matches

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A;Status: preliminary
A;Status: preliminary
A;Status: preliminary
A;Rotale type: DNA
A;Residues: 1-467 < KUR.
A;Reperimental source: strain 1021, megaplasmid pSymB
A;Experimental source: strain 1021, megaplasmid pSymB
B;Gallbert, F:; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler,
B;Gallbert, P; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.;
L.; Hyman, R.W.; Jones, T.
Science 293, 668-6672, 2001
L.; Hyman, R.W.; Vonelter, F.J.; Weidner, S.; Wells, D.H.; Kiss, E.; Komp, C.; Lelaure,
A;Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K.C
A;Title: The composite genome of the legume symbiont Sinorhizobium meliloti.
A;Reference number: A96039; MUID:21368234; PMID:11474104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Glypican precursor - rat
C;Species: Rattus norvegicus (Norway rat)
C;Species: Z6-Jul-1996 #sequence revision 26-Jul-1996 #text_change 31-Jan-2000
C;Accession: I56545; JC1281; FC1132
C;Accession: I56545; JC1281; FC1132
J. Neurosai: 14, 3713-3724, 1994
A;Title: Neuronal expression of glypican, a cell-surface glycosylphosphatidylinositol-and A;Reference number: I56545; MUID:94267529; FMID:8207484
A;Accession: I56545
A;Status: preliminary; translated from GB/EMBL/DDBJ
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R, Karthikeyan, L.; Maurel, P.; Rauch, U.; Margolis, R.K.; Margolis, R.U.
Biochem. Biophys. Res. Commun. 188, 39-7401, 1992
A, Title: Cloning of a major heparan sulfate proteoglycan from brain and identification as
                                                                                                                                                                                                                                                                                                                                                                                                                                                    probable amino acid carrier protein [imported] - Sinorhizobium meliloti (strain 1021) mag
C;Species: Sinorhizobium meliloti
C;Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 30-Sep-2001
C;Accession: E95850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RiFinan, T.M.; Weidner, S.; Wong, K.; Buhrmester, J.; Chain, P.; Vorholter, F.J.; Hernand Proc. Natl. Acad. Sci. U.S.A. 98, 9889-9894, 2001
A;Title: The complete sequence of the 1,683-kb pSymB megaplasmid from the N2-fixing endos A;Reference number: A95842; MUID:21396508; PMID:11481431
                                  5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7;
                                                                                                                                          49 ARDALRRVAFVRAAQRVGIPLATIREALAELPEGRIPTEDDWARLSESWRSELDERIKQL 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    322 LAIMVSGVWASGETGAVLSSAAFEAALPG----YGNYLVTISLALFAFTTILGWAYYAE 376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ----SWSADLD 47
                                                                                                2 ARGSIRRILRILV---LGLWLALLRSVAGEQAPGTAP----CSRGSSWSADLDKCMDCA
                                  26; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       43; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C, Superfamily: sodium-dependent D-alanine/glycine transport protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 26.4%; Pred. No. 26;
Matches 28; Conservative 14; Mismatches 21; Indels 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       409
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                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            48 KCMDCASCRARPHSDFCLGCAAAPPAPFRLLWPI---LGGALSLTF
                                                                                                                                                                                                                                                                                               -----GCLSLETCVL 131
                                                                                                                                                                                                                                54 SCRARPHSDFCLGCAAAPPAPFRLLWPILGGALSL-TFVL 92
                                  33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10 LRLLVLGLWL----ALLRSVAGEOA-PGTAPCSRGS---
   29.0%; Pred. No. 11; tive 12; Mismatches
                                                                                                                                                                                                                                                                             : | | | |:||
109 N-RLRDHLTDCIGC-----
                                  29; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Residues: 1-558 < RES>
      Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A, Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Accession: E95850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Gene: SMb20069
A;Genome: plasmid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C; Genetics
                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 14
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A;Molecule type: DNA
A;Residues: 1-346 <WHID-
A;Cross-references: GB:AE002053; GB:AE000513; NID:g6459999; PIDN:AAF11754.1; PID:g646000
A;Experimental source: strain R1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ge
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rivin, W.; Smiley, B.; Germiller, J.; Sanguineti, C.; Lawton, T.; Pereira, L.; Ramirez, J. Biol. Chem. 270, 1798-1806, 1995
A;Title: Primary structure and developmental expression of Fbn-1, the mouse fibrillin g. A;Reference number: A55624; MUID:95130561; PMID:7829516
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             probable transcription regulator soxR-like - Streptomyces coelicolor C; Species: Streptomyces coelicolor C; Species: Streptomyces coelicolor C; Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 07-Dec-1999 C; Accession: T36799 #sequence_revision 03-Dec-1999 #text_change 07-Dec-1999 R; Oliver, K.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A. submitted to the EMBL Data Library, July 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: EMBL:AL096811; PIDN:CAB46795.1; GSPDB:GN00070; SCOEDB:SCI30A.18c
A;Experimental source: strain A3(2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2040 CPEGFSWSSSGRRCQDLRMSYCYAKFEGGRCSSPKSRNHSKOECCALKGEGWGDPCELC 2099
                                                                                                                                                                                                                                                                                                                                     2
                                                                                                                                                                                                                                                                                                                                                                                                                                                              87 LLVTCVGLGVL--TAGSASPWTV-----MWVGALVAAFGAVLATVWHLRPAGSLFFVFA 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          67
                                                                                                                                                                                                                                                                                                                                                                                                12 LLVLGLWLALLRSVAGEQAPGTAPCSRGSSWSADLDKCMDCASC---RARPHSD----FC 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Species: Mus musculus (house mouse)
C;Date: 23-Mar-1995 #sequence_revision 23-Mar-1995 #text_change 24-Nov-2003
                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-2871 <YIN>
A;Cross-references: GB:L29454; NID:g575509; PIDN:AAA56840.1; PID:g575510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                65 LGCAAA--PPAPFRLLWPILGGALSLTFVLGLLSGFLVWRRCRRERSSPPP 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  139 VGTVGALPHPAPLPLALAVSGGAAALSVALGALGAWHSTRARPHELAAPPP 189
                                                                                                                                                                                                                                                                                                                                 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28;
                                                                                                                                                                                                                                                                   Length 346;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 72; DB 2; Length 2871;
Pred. No. 75;
7; Mismatches 24; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 2; Length 175;
                                                                                                                                                                                                                                                                                                                                 52; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     24; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -CASCRARPHS
                                                                                                                                                                                                                                                                   5;
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A;Molecule type: DNA
                                                                                                                                                                                                                                                                   DB
                                                                                                                                                                                                                                                            11.9%; Score 72.5; Di
28.8%; Pred. No. 13;
Live 10; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11.7%; Score 71;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2100 PTEPDEAFROICPFGSGII 2118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Superfamily: fibrillin; EGF homology F:1201-1236/Domain: EGF homology <EGF>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      68 AAAPPAPFRLLWPILGGAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     l Similarity 25.3%;
20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CSRGSSWSADLDKCMD
                                                                                                                                                                                                                                                                                                                              32; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 fibrillin-1 precursor - mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Reference number: Z21614
A;Accession: T36798
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A, Gene: SCOEDB: SCI30A.18c
                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 20; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1-175 <OLI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Accession: A55624
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Accession: A55624
                                                                                                                            C;Genetics:
A;Gene: DR2205
A;Map position: 1
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36

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RESULT 12

Query Match

Genetics:

A; Residues:

A; Gene: Fbn-1

Genetics:

A; Reference number: JC1281; MUID: 93038690; PMID: 1417860

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A; Molecule type: protein
A; Residues: 24-55;424-445 < KR2>
A; Residues: 24-55;424-445 < KR2>
C; Superfamily: glypican
C; Superfamily: glypican
C; Reywords: blocked carboxyl end; chondroitin sulfate proteoglycan; glycoprotein; hepara
C; Reywords: blocked carboxyl end; predicted <81G>
F; 1-23/Domain: signal sequence #status predicted <MAT>
F; 24-530/Product: glypican #status predicted <MAT>
F; 530/Product: glypican #status predicted *Ratus predicted <CTP>
F; 55-486, 488, 490/Binding site: carboxyl-terminal propeptide #status predicted
F; 79, 116/Binding site: carbohydrate (Mrx) (covalent) #status predicted
F; 399, 512/Binding site: carbohydrate (Thr) (covalent) #status predicted
F; 530/Modified site: GPI-anchor ethanolamine amidated carboxyl end (Ser) (in mature form
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C.Accession: D75330
R;White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;
M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Ma
S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571_1577, 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cross-references: GB:AE002036; GB:AE000513; NID:g6459766; PIDN:AAF11537.1; PID:g645977
Experimental source: strain R1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1. Reference number: A75250; MUID:20036896; PMID:10567266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     221 RSFVQGLGVASDVVRKVA--QVPLAPECSRA-----VMKLVYCAHCRGVPGARPCPDYC 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3 RGSLRRLLRLLVLGLWLALLRSVAGEQAPGTAPCSRGSSWSADLDKCMDCASCRA---- 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 RGTIRLTLALLLIG---AGINACRNREAQDTAPPAAAAAQSQAAPRKAASASSPAPTATE 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Species: Deinococcus radiodurans
;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 31-Mar-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11 RLLVLGLWLA---LLRSVAGEQAPGTAPCSRGSSWSADLDKCMDCASCR----ARPHSDFC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18; Gaps
;Molecule type: mRNA
;Residues: 1-20,'T',22-311,'Y',313-361,'A',363-514,'I',516-558 <KAR>
;Cross-references: GB:L02896; NID:g204424; PIDN:AAA86439.1; PID:g204425
;Experimental source: brain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 70; DB 2; Length 558;
Pred. No. 33;
6; Mismatches 19; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      probable beta-lactamase - Deinococcus radiodurans (strain R1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  58 ----RPHSDFCLGCAAA-----PPAPFRLLWPILGGALSL 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -----LSGRLGL 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 69.5; DB 2;
Pred. No. 30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11; Mismatches
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ne: 43 secs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cn 11.5%;
1 Similarity 37.7%;
26; Conservative (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               273 RNVLKGCLA 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ---- LGCAA 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 26; Conserv
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Status: preliminary
Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A, Accession: D75330
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Search comp Job time :

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GenCore version 5.1.6
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OM protein - protein search, using sw model

March 1, 2004, 16:37:03 ; Search time 17 Seconds (without alignments) 349.176 Million cell updates/sec Run on:

Title: Perfect score:

US-10-062-599-59 608 1 MARGSLRRLLRLAULGLWLA......LSGFLVWRRCRRBRSSPPPX 114

Scoring table: Sequence:

141681 seqs, 52070155 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries

SwissProt_42:* , Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		Description	Q9np84 homo sapien	Q9cr75 m tumor nec	Q96rj3 homo sapien		Q9wvh9 mus musculu	P54700 salmonella	Q8k406 mus musculu	P56815 methanobact	015118 homo sapien	_	Q9uja2 homo sapien	Q9wvj9 mus musculu	P35053 rattus norv	Q24400 drosophila	homod		rattı	015499 homo sapien	_	Q9bzj7 homo sapien		P54755 gallus gall		Q63072 rattus norv	Q62424 mus musculu	P54757 rattus norv		O55058 cricetulus	P42514 pseudomonas		Q9y219 homo sapien	_	ratt
SUMMARIES	f			FN14 MOUSE	T13C HUMAN	FBL5 RAT	FBL5 MOUSE	FLIP_SALTY	LGI3 MOUSE	PORD_METTH	NPC1 HUMAN	FBN1 MOUSE	CTF5 HUMAN		GPC1_RAT	MLP2 DROME	PTTG HUMAN		TNR6 RAT	GSCL HUMAN	YG84 METTH	GP62 HUMAN	VGLM_UUK	EPA5_CHICK	CXE1_HUMAN	BST1_RAT	HXAD MOUSE	EPAS_RAT		FBL4 CRIGR	Y6B9 PSEAE	POLS_RUBVM	JAG2 HUMAN		NTC3_RAT
	ţ	9 !	Н	Н	н	Н	_	႕	Н	Н	Н	Н	Н	Н	Н	Н	Н	Н	Н	Н	Н	Н	н					٦	Н	٦	٦	-	-	н	н
	1	rengun	129	129	184	448	448	245	548	81	1278	2871	301	443	558	495	180	314	324	205	431	368	1008	1013	279	319	386	1005	2871	443	394	992	1238	2318	2319
sk		MACCII	93.9		14.3	12.8	12.7	12.6	12.2	12.1	11.8	11.8	11.5	11.5	11.5	11.4	11.3	11.3	11.3	11.3	11.3	11.1	11.1	11.1	11.0	11.0	11.0	11.0	11.0	10.9	0	0	10.9	10.9	10.9
	0	2005	571	445	87	78	77	76.5	74	73.5	72	72	70	70	70	69.5	69	69	69	68.5	68.5	67.5	67.5	67.5	67	67	67	49	9	66.5	99	99		99	99
	Result		Н	7	e	4	ഗ	9	7	œ	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23			56	27	28	29	30	31	32.	33

				P23470 homo sapien							
FLIP ECOLI	NTC3 HUMAN	HRA3 HUMAN	EPB6 MOUSE	PTPG HUMAN	PLA8 MOUSE	VST1 HEVME	TREB HUMAN	FBL4 HUMAN	PLA8 HUMAN	EGFR MOUSE	B3A3_MOUSE
Н	-	Н	Н		Н	Н	٦	٦	Н	н	Н
245	2321	453	1014	1445	112	123	300	443	115	1210	1227
10.8	10.8	10.7	10.7	10.7	10.6	10.6	10.6	10.6	10.5	10.5	10.5
	S	65	65	65	54.5	64.5	64.5	64.5	64	64	64
65.5	65.				•						

ALIGNMENTS

RESULT 1

FN14	1 1 1
D FC	Q9NP84; Q9HCS0; 28-FEB-2003 (Rel. 41, Created)
占	(Rel. 41, Last
DŢ	10-OCT-2003 (Rel. 42, Last annotation update)
O C	Tumor necrosis factor receptor superfamily member Fn14 precursor
3 E	
GN	4
SO	. (
9.8	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
ŏ	
Z Z	[1] SECUENCE FROM N.A. (ISOFORM 1).
RC	TISSUE=Placenta;
ž :	
5 5	reng sb.i., euc i., ractor v.m., inorgelisson s.s., bell D.w., Testa I R. Deiflav K & Winkles I A .
R.	"The Fn14 immediate-early response gene is induced during liver
RT	in both human and murine
RT	atocellular
2	Am. J. Pathol. 156:1253-1261(2000).
Z 6	(2)
7 C	LISOFORMS I MAND
§ 5	Idinas of Colimon of Frie
Z Z	Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
Z.	
RP	SEQUENCE FROM N.A. (ISOFORM 1).
۲ ا	TISSUE-Uterus;
ž	MEDLINE=22388257; Pubmed=12477932;
\$ 2	Strausberg K.L., Feingold E.A., Grouse L.H., Derge J.G.,
5 6	Alausher K.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
S &	Arrector J. J. J. Decoder J. J. J. J. J. J. J. J. J. Hailer F. J. Jordan H. Moore T. Mark S. T. Wang J. Haileh F.
R.	Distribution K. Farmer A. Rubin G.M. Hond L.
RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA	Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
R.A	Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
8 2	Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
§ :	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
¥ 5	ŧ
Z Z	Famey o., metrom E., Aetremman M.C., Madam A., Kourigues S., Samonez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA A	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA:	Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
A F	Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.; "Caneration and initial analysis of more than 15 000 full-length
RT	and mouse cDNA sequences.";
Z Z	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
2 H	PUNCTION.

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                Wiley S.R., Cassiano L., Lofton T., Davis-Smith T., Winkles J.A., Lindner V., Liu H., Daniel T.O., Smith C.A., Fanslow W.C.; "A novel TNF receptor family member binds TWEAK and is implicated in anglogenesis.";
                                                                                                                                                                                                                                                                               proteins.
SUBUNIT: Associates with TRAF1 and TRAF2, and probably also with
                                                                                                                                               Immunity 15:837-846(2001).
-!- FUNCTION: Receptor for INFSF12/TWEAK. Weak inducer of apoptosis
-!- FUNCTION: Receptor for INFSF12/TWEAK. Weak inducer of apoptosis some cell types. Promotes angiogenesis and the proliferation of endothelial cells. May modulate cellular adhesion to matrix
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE SPECIFICITY: Highly expressed in heart, placenta and kidney. Intermediate expression in lung, skeletal muscle and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TUMOR NECROSIS FACTOR RECEPTOR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Receptor, Angiogenesis; Apoptosis, Transmembrane, Signal; Alternative splicing.
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13911 MW; BF3FDFB9C1E1C448 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                    -!- SUBCELLULAR LOCATION: Type I membrane protein.
-!- ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                     Event=Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFR-CYS (ATYPICAL)
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Pred. No. 2.8e-48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INDUCTION: By FGF-1 and phorbol ester. SIMILARITY: Contains 1 TNFR-Cys repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IsoId=09NP84-2; Sequence=VSP 006519;
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GO; GO:0006928; P:cell motility; TAS.
GO; GO:0007275; P:development; TAS.
InterPro; IRR001368; TNFR. GO:
PROSITE; PS00652; TNFR. NGFR. 1; FALSE NEG.
PROSITE; PS50050; TNFR. NGFR. 2; FALSE_NEG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IsoId=09NP84-1, Sequence=Displayed;
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MEDLINE=21585797; PubMed=11728344;
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EMBL; AB035480; BAA94792.1; -.
EMBL; AB035481; BAB17450.1; -.
EMBL; BC002718; AAH02718.1; -.
Genew; HGNC:18152; TNFRSF12A.
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MININGERIAL STRIBE—Correbellum, and Placenta;

MEDINE=21086660; PubMed=11217851,

RAMARIA T., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

RAMARWA T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,

Alawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

RAMARA Saito T., Okazaki Y., Gojobori T., Bono H., Radukawa T., Saito R.,

Radota K., Matsuda H.A.; Ashburner M., Batalov S., Casavant T.,

Radota K., Matsuda H.A.; Ashburner M., Batalov S., Casavant T.,

RAMARIA S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

Ruehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

Rochim L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,

RAMARIA S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,

RAMARIA S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,

RAMARIA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,

RAMARIA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,

RAMARIA SAN Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,

Whynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,

RAMARIA SANDARA SANDARA SANDA SANDA SANDA COllection.",

Natura M., Matali M., Matali M., Roding C., Whittaker C., Wilming T.,

RAMARIA SANDA SANDA SANDA SANDA SANDA COllection.",

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MEDLINE=223825; PubMed=12477932;

MEDLINE=223825; PubMed=12477932;

MEDLINE=223825; PubMed=12477932;

MALSTONE R.D., Colling F.S., Wagner L., Sheamen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Altschul M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Arabes S.J., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Raha S.S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Willalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Willalon B., Ketteman M., Madan A., Rodrigues S., Sanchez A., Mitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Malkealey R.W., Touchman J.W., Green E.D., Dickson M.C., Blakealey R.W., Touchman J.W., Stabaka U., Smailus D.E., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Content A., Schein J.E., Jones S.J.M., Marra M.A.; Schein J.E., Schein J.E., Schein J.E., Sone E. S., M., Marra M.A.; Schein J.E., Sone E. S., M. Marra M.A.; Schei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
STRAIN=BALB/C; TISSUB=Fibroblast;
MEDLINE=20002097; PubMed=1055188;
MEDLINE=20002097; PubMed=1055188;
Meighan-Martha R.L., HSU D.K.W., Guo Y., Brown S.A.N., Feng S.-L.Y.,
Peifley K.A., Alberts G.F., Copeland N.G., Gilbert D.J., Jenkins N.A.,
Richards C.M., Winkles J.A.;
"The mitogen-inducible Fn14 gene encodes a type I transmembrane
protein that modulates fibroblast adhesion and migration.";
J. Biol. Chem. 274:33166-33176(1999).
                    096775; 0902W3;
28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
10-0672-2003 (Rel. 42, Last annotation update)
Tumor necrosis factor receptor superfamily member Fn14 precursor (Fibroblast growth factor-inducible immediate-early response protein 14) (FGF-inducible 14) (Ribroblast growth factor regulated protein 2)
                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
129 AA
PRT;
                                                                                                                                                                                                                                                   (Tweak-receptor) (TweakR).
INFRSF12A OR FU14 OR FGFRP2.
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STANDARD;
                                                                                                                                                                                                                                                                                                                    Mus musculus (Mouse)
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FN14 MOUSE
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Gaps

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6; Indels

0; Mismatches

94.78;

Matches 107; Conservative

1 MARGSLRRLLRLLVLGLWLALLRSVAGEQAPGTAPCSRGSSWSADLDKCMDCASCRARPH 1 MARGSLRRLLRLLVLGLWLALLRSVAGEQAPGTAPCSRGSSWSADLDKCMDCASCRARPH

SDFCLGCAAAPPAPFRLLWPILGGALSLTFVLGLLSGFLVWRRCRRERSSPPP 113 61 SDFCLGCAAAPPAPFRLLWPILGGALSLTFVLGLLSGFLVWRRCRRREKFTTP 113

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                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AF156164; AAF07882.1; --
EMBL; AK005302; BAB24101.1; --
EMBL; AK005302; BAB24101.1; --
EMBL; AK005302; BAB22899.1; --
EMBL; BC025866; AAH25860.1; --
MGD; MG1:1351484; Tnfref12a.
MGD; MG1:005886; Crplamam membrane; IDA.
GO; GO:0007155; P:cell adhesion; IDA.
GO; GO:0007155; P:cell adhesion; IDA.
FROSITE; PS0652; TNFR GC.
PROSITE; PS0652; TNFR MGFR I; FALSE NEG.
PROSITE; PS0652; TNFR NGFR I; FALSE NEG.
FRECEPLOT; Anglogenesis; Apoptosis; Transmembrane; Signal.
               of apoptosis in some cell types. Promotes angiogenesis and the proliferation of endothelial cells. May modulate cellular adhesion to matrix proteins.
Receptor for INFSF12/TWBAK (By similarity). Weak inducer
                                                                  -!- SUBUNIT: Associates with TRAF1 and TRAF2, and probably also with TRAF3 (By similarity)
-!- SUBCELLULAR LOCATION: Type I membrane protein.
-!- TISSUE SPECIFICITY: Highly expressed in fetal heart, intestine, kidney, liver, lung and skin, and in adult heart and ovary. Intermediate expression in adult kidney, lung and skin.
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                                                                                                                                                                                INDUCTION: By FGF-1.
SIMILARITY: Contains 1 TNFR-Cys repeat.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS00652; TNFR NGFR 1; FALSE NEG.
PROSITE; PS50050; TNFR_NGFR_2; FALSE_NEG.
Receptor; Immune response; Signal-anchor; Transmembrane;
Alternative splicing; 3D-structure.
DOMALN
TRANSMEM 79 99 SIGNAL-ANCHOR
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BY SIMILARITY.
BY SIMILARITY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AF373846; AAK91826.1; -. PDB; 1MPV; 30-OCT-02. Genew; HGNC:17755; INFRSF13C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR001368; INFR c6.
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MASAWPRSIPOILVLGFGLVIMRAAAGEQAPGTSPCSSGSSWSADLDKCMDCASCPARPH 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28-FEB-2003 (Rel. 41, Last sequence update)
LOCT-2003 (Rel. 42, Last annotation update)
Tumor necrosis factor receptor superfamily member 13C (B cellactivating factor receptor) (BAFF receptor) (BAFF-R) (BLyS receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SDFCLGCAAAPPAPFRLLWPILGGALSLTFVLGLLSGFLVWRRCRRERSSPPP 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 445; DB 1; Length 129;
Pred. No. 3.6e-36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SA -> PG (IN REF. 1).
1665C68B4D9A9253 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    184 AA
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(Rel. 41, Last seg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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Similarity

Query Match

Best Local

Matches

à d à g

84;

19

Homo sapiens (Human)

28-FEB-2003 T13C HUMAN

Q96RJ3;

RESULT 3 T13C HUMAN

NCBI_TaxID=9606;

9

Gaps

40;

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Note=No experimental confirmation available; TISSUE SPECIFICITY: Highly expressed in spleen and lymph node, and in resting B-cells. Detected at lower levels in activated B-cells, resting CD4+ T-cells, in thymus and peripheral blood leukocytes. SIMILARITY: Contains 1 TNFR-Cys repeat.

MEDLINE=21475520; PubMed=11591325; Yan M., Brady J.R., Chan B., Lee W.P., Hsu B., Harless S.M., Yan M., Brady J.R., Chan B., Lee W.P., Hsu B., Harless S.M., Lentron M.P., Grewal I.S., Dixit V.M.;
"Identification of a novel receptor for B lymphocyte stimulator that is mutated in a mouse strain with severe B cell deficiency.";
-1. FUNCTION: B-cell receptor specific for TNFSF13B/TALLI/BAFF/BLyS. Promoces the survival of mature B-cells and the B-cell response.
-1. SUBCELDULAR LOCATION: Type III membrane protein (Probable).

Event=Alternative splicing; Named isoforms=2;

lsoId=Q96RJ3-2; Sequence=VSP_006505; IsoId=Q96RJ3-1; Sequence=Displayed;

Ambrose C.; "BAPF-R, a newly identified TNF receptor that specifically interacts

Science 293:2108-2111(2001).

FUNCTION

with BAFF

Thompson J.S., Bixler S.A., Qian F., Vora K., Scott M.L., Cachero T.G., Hession C., Schneider P., Sizing I.D., Mullen C., Strauch K., Zafari M., Benjamin C.D., Tschopp J., Browning J.L.,

(ISOFORMS 1 AND 2)

FROM N.A.

TISSUE=B-cell lymphoma; MEDLINE=21442025; PubMed=11509692;

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SEQUENCE FROM N.A.
MEDLINE=99357779; Pubmed=10428823;
                                                                                                                                                                                                                                                                                                                                                                                                                                    S0160 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity 24.1%;
nes 26; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4 LKRILTVTILALWL----
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Mus musculus (Mouse)
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238
248 AA;
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                                                                                              DISULFID
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DOMAIN
DOMAIN
DOMAIN
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
MEDLINE=99278197; PubMed=10347091;
Kowal R.C., Richardson J.A., Miano J.M., Olson B.N.;
Kowal R.C., a novel epidermal growth factor-like repeat-containing protein upregulated in embryonic and diseased adult vasculature.";
circ. Res. 84:1166-1176(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FIBULIN-5.
EGF-LIKE 1, DIVERGENT.
EGF-LIKE 2, CALCIUM-BINDING (POTENTIAL).
EGF-LIKE 3, CALCIUM-BINDING (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                 Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                      Q9WVH8; Q9R284;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Fibulin-5 precursor (FIBL-5) (Developmental arteries and neural cres
EGF-like protein) (Dance) (Embryonic vascular EGF repeat-containing
FBLNS OR DANCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FUNCTION: Promotes adhesion of endothelial cells through interaction of integrins and the RGD motif. Could be a vascular ligand for integrin receptors and may play a role in vascular
                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
MEDLINE=99357779; PubMed=10428823;
MAEDLINE=99357779; PubMed=10428823;
Nakamwa T., Ruiz-Lozano P., Lindner V., Yabe D., Taniwaki M.,
Furukawa Y., Kobuke K., Tashiro K., Lu Z., Andon N.L., Schaub R.,
Matsumori A., Sasayama S., Chien K.R., Honjo T.;
Matsumori A., Sasayama S., Chien K.R., Honjo T.;
and balone secreted RGD procein expressed in developing,
atherosclerotic, and balloon-injured arteries.";
J. Biol. Chem. 274:22476-22483(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PS00010; ASX HYDROXYL; 4.
PROSITE; PS00022; BGF_1; FALSE_NEG.
PROSITE; PS010186; BGF_2; 4.
PROSITE; PS50026; BGF=3; 5.
PROSITE; PS01187; BGF_CA; 6.
Cell adhesion; Calcium-binding; Repeat; Signal; BGF-like domain;
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EMBL, AF137350; AAD2510.1; -.
HSSP, P00736; 1APQ.
INCEPPO; IPR00152; Asx hydroxyl_S.
INCEPPO; IPR01881; EGF_Ca.
INCEPPO; IPR001881; EGF_Ta.
Fam.; PF00008; EGF, 4
SMART; SM00179; EGF_CA; 4.
                                                                                                                                                          STANDARD;
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448
69
167
206
                      108 RSSPPP 113
                                                         121 KDAPEP 126
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24
127
168
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MEDLINE-22388257; PubMed=1247932;
MEDLINE-22388257; PubMed=1247932;
MEDLINE-22388257; PubMed=1247932;
MEDLINE-22388257; PubMed=1247932;
MISTER R.L., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.L., Wang J., Hsieh F.,
Diatchenko L., Marusina K., Parmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownsfein M.J., Usdin T.B., Toshhyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
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16-OCT-2001 (Rel. 40, Last sequence update)
15-DAR-2004 (Rel. 43, Last annotation update)
Fibulin-5 precursor (FIBL-5) (Developmental arteries and neural crest
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6 LRRLLRLLVLGLWLALLRSVAGEQAPGTA--PCSRGSSWSADLDKCMDCASCRARPHSDF
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                                                                                  (POTENTIAL).
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           CALCIUM-BINDING (POTENTIAL)
                                                (POTENTIAL)
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
EGF-LIKE 4, CALCIUM-BINDING (POTEN)
EGF-LIKE 5, CALCIUM-BINDING (POTEN)
EGF-LIKE 6, CALCIUM-BINDING (POTEN)
EGF-LIKE 6, CALCIUM-BINDING (POTEN)
EGL ATTACHMENT SITE (POTENTIAL).
BY SIMILARITY.
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N-LINKED (GLCNAC. . .) (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            53 CRGDMMCVNONGGYLCIPRTNPVYRGPYSNPYSTSYSGPYPAAAPPVP 100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12.8%; Score 78; DB 1; Length 448; 24.1%; Pred. No. 2.2; ...; Mismatches 24; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -> P (IN REF. 2).
EGBC68F7BF14B714 CRC64;
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Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Youchman M., Green E.D., Dickson M.C., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schain J.E., Jones S.J.M., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R HSSP; P00736; 1APA.

R HSSP; P00736; 1APA.

R MGD; MGI:1346091; Fbln5.

R InterPro; 1PR001629; BGF Ca.

R InterPro; 1PR00181; EGF Ca.

R FORSTE; PS00109; EGF CA; 4.

R PROSITE; PS01166; EGF CA; 4.

R PROSITE; PS01166; EGF CA; 4.

R PROSITE; PS01166; EGF CA; 4.

R PROSITE; PS01167; EGF CA; 4.

R PROSITE; PS01187; EGF CA; 6.

R Call adhesion; Calcium-binding; Repeat; Signal; EGF-like domain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (POTENTIAL)
                                                                                                                                                                                                                                             Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
-!- FUNCTION. Promotes adhesion of endothelial cells through interaction of integrins and the RGD motif. Could be a vascular ligand for integrin receptors and may play a role in vascular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FIDULIN'S

FIGURAN'S

EGF-LIKE 1, DIVERGENT.

EGF-LIKE 3, CALCIUM-BINDING (POTENT

EGF-LIKE 4, CALCIUM-BINDING (POTENT

EGF-LIKE 6, CALCIUM-BINDING (POTENT

EGF-LIKE 6, CALCIUM-BINDING (POTENT

EGF-LIKE 6, CALCIUM-BINDING (POTENT

EGF-LIKE 7, CALCIUM-BINDING

EGF-LIKE 7, CALCIUM
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N-LINKED (GLCNAC. . .) (POTENTIAL)
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F15CC70CCFBFDC97 CRC64;
                                                                                                                                                                                                                                                                                                                                            development and remodeling.

--- SUBCELLULAR LOCATION: Secreted.

--- SIMILARITY: Belongs to the fibulin family.

--- SIMILARITY: Contains 6 EGF-like domains.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AF112151; AAD41767.1; -.
EMBL; BC006636; AAH06636.1; -.
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24.1%;
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262
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138
155
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217
232
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SIGNAL
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DISULFID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
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DOMAIN
DOMAIN
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Length 448;

DB 1;

Best Local Similarity

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5
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                                                                    6 LRRLLRLLVLGLWLALLRSVAGEQAPGTA--PCSRGSSWSADLDKCMDCASCRARPHSDF 63
                                                                                                                                        52
                                                                                                                                        --PHPGNAQQCTNGFDLDRQSGQCLDIDECRTIPEA--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=21534948; PubMed=11677609;
McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P.,
Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D.,
Leonard S., Mayuen C., Scott K., Holmes A., Grewal N., Mulvaney E.,
Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M.,
Waterston R., Wilson R.K.;
"Complete genome sequence of Salmonella enterica serovar Typhimurium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nature 413:852-856(2001).
-!- FUNCTION: Plays a role in the flagellum-specific transport system
(By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -!- SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane.
-!- MISCELLANBOUS: For insertion of flip into the membrane, cleavage
of the signal peptide is important kinetically but not absolutely
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ohnishi K., Fan F., Schoenhals G.J., Kihara M., Macnab R.M.; The Filo, Filo, and Filk proteins of Salmonella typhimurium: putative components for flagellar assembly."; J. Bacteriol. 179:6092-6099(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales,
                                                                                                                                                                                                                                                                        53 CRGDMMCVNQNGGYLCIPRINPVYRGPYSNPYSTSYSGPYPAAPPVP 100
                                                                                                                                                                                                        74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SIMILARITY: BELONGS TO THE FLIP/MOPC/SPAP FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PS01061; FLIP_2; 1.
Flagellum; Transmembrane; Inner membrane; Transport;
   24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A., AND SEQUENCE OF N-TERMINUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-0cT-1996 (Rel. 34, Created)
01-0cT-1996 (Rel. 34, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Flagellar biosynthetic protein flip precursor.
Salmonella typhimurium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    245 AA
   8; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
SCHILL / SCHILL / ATCC 700720;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=97464436; PubMed=9324257;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Enterobacteriaceae; Salmonella.
NCBI_TaxID=602;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRINTS; PR01302; TYPE3IMPPROT. ProDom; PD002586; TYPEIII P; 1. TIGRFAMS; TIGR01103; flip; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR005837; Flip.
InterPro; IPR005838; TypeIII_P.
Pfam; PF00813; Flip; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; L49021; AAB81319.1; -.
EMBL; AE008787; AAL20891.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE; PS01060; FLIP 1; 1.
PROSITE; PS01061; FLIP 2; 1.
                                                                                                                                                                                             64 CLG-----C-
26; Conservative
                                                                                                                                    4 LKRILTVTILALWL--
                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PIR; S78698; S78698.
StyGene; SG10577; fliP.
                                                                                                                                                                                                                                                                                                                                                                                                         FLIP SALTY
ID FLIP SALTY
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Matches
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SETABLE C. TISSUE=Hippocampus;

MEDLINE=22354683; PubMed=12466851;

MEDLINE=22354683; PubMed=12466851;

A OKAZARI Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,

AN ARAIGO I., Osato N., Salto R., Suzuki H., Yamanaka I., Kiyosawa H.,

RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,

Schriml L.M., Kanapin A., Bult C., Hume D.A., Quackenbush J.,

Schriml L.M., Ranapin A., Batchor C.F., Forrest A., Fazzer K.S.,

Bake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,

Bake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,

Bake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,

RA Balas E., Dragani T.A., Fatcher C.F., Forrest A., Fazzer K.S.,

Garsterland T., Gariboldi M., Gissi C., Godzik A., Guyh J.,

Garsterland T., Gariboldi M., Gissi C., Lenhard B.L., Marvis E.D.,

RA Magnott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,

RA Nagashima T., Numata K., Okido T., Pavan W., Pertra G., Pescole G.,

Petrovsky N., Pollial R., Pontius J.U., Qi D., Ramachandran S.,

Petrovsky N., Schneider C., Semple C.A., Secou M., Shimada K.,

Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,

Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,

Sultana R., Waki K., Kawai J., Aizawa K., Arakawa T., Pukuda S.,

Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,

RA, Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,

RA, Milmish L.G., Watshizaki Y., Sasaki D., Shibata K., Shinagawa A.,

Hara A., Hashitume W., Ilmotani K., Ishii, Y., Itoh M.,

Binney E., Hayashizaki Y.,

Binney E., Hayashizaki Y.,

Ballaki Y., Shinagawa A.,

Ballaki 
                                                                                                                                                                                                                                                                                                  6 LRRLLRLLVLGLWLALLRSVAGEQAPG--TAP-CSRGSSWSADLDKCMDCASCRARP--- 59
                                                                                                                                                                                                                                                                                                                                              1 MRRLLFLSLAGLW--LFSPAAAAQLFGLISQPLAGGGQSWSLSVQTLVFITSLTFLFAIL 58
                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                FLAGELLAR BIOSYNTHETIC PROTEIN FLIP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10-0cT-2003 (Rel. 42, Created)
10-0CT-2003 (Rel. 42, Last sequence update)
15-MR-2004 (Rel. 43, Last annotation update)
Leucine-rich repeat LGI family member 3 precursor (Leucine-rich glioma-inactivated protein 3) (Leubrin).
                                                                                                                                                                                                                                                       27;
                                                                                                                                                                                                         12.6%; Score 76.5; DB 1; Length 245; 30.8%; Pred. No. 1.8;
                                                                                                                                                                                                                                                                                                                                                                                                                                       59 LMMTSFTRIIIVFGLLRNALGTPSAPPNQV----LLGLALFLTFFI 100
                                                                                                                                                                                                                                                                                                                                                                                           --CLGCAAAPPAPFRLLWPILGGALSLTFVL 92
                                                                                                                                                                                                                                                       38; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=BALB/c; TISSUE=Brain;
Yun H.-Y., Lee S.E.;
Submitted (NOV-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                              C9A4241F0653A4D4 CRC64;
Protein transport; Signal; Complete proteome.
SIGNAL
CHAIN
22 245 FLAGELLAR BIOSYN
TRANSMEM 48 65 POTENTIAL.
TRANSMEM 88 108 POTENTIAL.
TRANSMEM 185 205 POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          548 AA
                                                                                                                                                                                                                                                       9; Mismatches
                                                                                                                                      POTENTIAL
                                                                                                                                                            26787 MW;
                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                               245
65
108
2205
229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus (Mouse)
                                                                                                                                                              245 AA;
                                                                                                                                                                                                                               Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=10090;
                                                                     45
88
185
209
                                                                                                                                                                                                                                                     33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LGI3_MOUSE
ID LGI3_MOUSE
AC Q8K406;
                                                                                                                                                                                                         Query Match
                                                                                                                                                            SEQUENCE
                                                                                                                                        TRANSMEM
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration
                                          SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

MICHINE-257BL/6; TISSUB-Brain;

Altacher R.D., Feingold E.A., Grouse L.H., Derge J.G.,

Rausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

Altachul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heich F.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Rapleton M., Soares M.B., Bonaldo M.F., Carninci P., Prange C.,

Brownstein M.J., Usdin T.B., Tooshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Raba S.S., McEwan P.J., McKernan K.J., Malek J.A., Guaratane P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Whiting M., Madan A., Young A.C., Shewchenko Y., Bouffard G.G.,

Rakesley W., Helton B. Ketteman M., Madan R.D., Dickson M.C.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Redriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

"Generation and initial analysis of more than 15,000 full-length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LEUCINE-RICH REPEAT LGI FAMILY MEMBER 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-LINKED (GLCNAC. . .) (POTENTIAL)
N-LINKED (GLCNAC. . .) (POTENTIAL)
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POTENTIAL.
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LERR 4.
LERR 5.
EAR 1.
EAR 2.
EAR 3.
EAR 4.
EAR 5.
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InterPro; IPR005492; EAR.
InterPro; IPR001611; LRR.
InterPro; IPR001611; LRR.
InterPro; IPR000483; LRR_Cterm.
InterPro; IPR003591; LRR_typ.
Pfam; PF00463; EAPP; 2.
Pfam; PF00466; LRR; 3.
Pfam; PR00463; LRRCT; 1.
SMART; SM00369; LRR_TYP; 3.
SMART; SM00369; LRR_TYP; 3.
PR051TE; PS50912; EAR; 6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL, AF515590; AAM55219.1; -.
EMBL, AX174677; AA019739.1; -.
EMBT. AX049831; BAC33943.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; BC055315; AAH55315.1; -. EMBL; BC061460; AAH61460.1; -. MGD; MGI:2182619; Lgi3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61817 MW;
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Nature 420:563-573 (2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          548 AA;
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135
160
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CARBOHYD
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   SOLUTION OF THE PROPERTY OF TH
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Length 548;

DB 1;

Score 74;

12.2%;

Query Match

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SEQUENCE FROM N.A., AND VARIANTS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Science 277:228-231 (1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hum. Mutat. 19:30-38(2002)
                                                                                                                                                                                                                                                                                                                                      (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VARIANT NPD TRP-992.
                                                                                           PFRLL 78
                                                                                                                          PVKAI 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CHARACTERIZATION,
                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         homeostasis.
                                                        11
                                                                                           74
                         31
                                                                                                                                                                              RESULT
                                                    d
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                                                                                                                                                                                                                                  6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              deltaH: functional analysis and comparative genomics.",
J. Bacteriol. 179:7135-7155(1997)
-!- CATALYTIC ACTIVITY: Pyruvate + CoA + oxidized ferredoxin = acetyl-
CoA + CO(2) + reduced ferredoxin.
-!- COFACTOR: Binds 2 4Fe-45 clusters.
-!- SUBUNIT: Heterotetramer of one alpha, one beta, one delta and one
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -!- SIMILARITY: Belongs to the bacterial-type ferredoxin family.
-!- CAUTION: THERE SEEMS TO BE A SEQUENCING ERROR THAT FUSES TOGETHER
PORC AND PORD. WE HAVE CUT THE ORF INTO ITS TWO CONSTITUENTS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Smith D.R., Doucette-Stamm L.A., Deloughery C., Lee H.-M., Dubois J., Aldredge T., Bachirzadeh R., Blakely D., Gook R., Gilbert K., Haarison D., Hoang L., Keagle P., Lumm W., Pothier B., Qiu D., Spadafora R., Vicare R., Wang Y., Wierzbowski J., Gibson R., Jiwani N., Caruso A., Bush D., Safer H., Patwell D., Prabhakar S., McDougall S., Shimer G., Goyal A., Pietrovski S., Church G.M., Baniels C.J., Mao J.-I., Rice P., Noelling J., Reeve J.N., "Complete genome sequence of Methanobacterium thermoautotrophicum
                                                                                                                                                                                                          30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Pyrruvate synthase subunit porD (EC 1.2.7.1) (Pyruvate oxidoreductase delta chain) (POR) (Pyruvic-ferredoxin oxidoreductase delta subunit).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                    3 RGSLRRLLRLLVLGLWLALLRSVAGEQAPGTAPCSRGSSWSADLDXCMDCAS 54
                                                                          Pfam; PF00037; fer4; 2. --
PROSITE; PS00198; 4PE4S_FERREDOXIN; 2.
Oxidoreductase; Electron transport; Iron-sulfur; Repeat; 4Fe-4S;
                       2;
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                                                                                                                                                                                                                                                                                                                                    Archaea; Buryarchaeota; Methanobacteria; Methanobacteriales; Methanobacteriaceae; Methanothermobacter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 73.5; DB 1; Length 81;
                     Indels
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IRON-SULFUR 1 (4FE-4S) (1

IRON-SULFUR 2 (4FE-4S) (1

IRON-SULFUR 1 (4FE-4S) (1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       219A9CCAE8A41604 CRC64;
                    24;
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                                                                                                                                                                              81 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8; Mismatches
                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   entities requires a license agreement (Sor send an email to license@isb-sib.ch).
     Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR001450; 4Fe48_ferredoxin.
                                                                                                                                                                                                                                                                                                                    Methanobacterium thermoautotrophicum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AE000929; AAB86210.1; ALT_INIT. HSSP; P00195; 1CLF.
                                                                                                                                                                           PRT;
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                    5,
   40.48;
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29.2%;
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                    21; Conservative
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Best Local Similarity 29.2
Matches 19; Conservative
                                                                                                                                                                             STANDARD;
Best Local Similarity
Matches 21; Conserv
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63
66
70
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SOLUTION SOLUTION STATEMENT OF SOLUTION SOLUTION

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PGTAPCSRGSSWSA----DLDKCMDCASCRA-----RPHS---DFCLGCA-AAPPA 73
                                                   MEDINE=97362323; PubMed=9211849;
MEDINE=97362323; PubMed=9211849;
Carstea B.D., Morris J.A., Coleman K.G., Loftus S.K., Zhang D., Cummings C., Gu J., Rosenfeld M.A., Pavan W.J., Krizman D.B., Magle J., Polymeropoulos M.H., Sturley S.L., Ioannou Y.A., Higgins M.E., Conly M., Cooney A., Brown A., Kaneski C.R., Liscum L., Strauss J.F. III, Ohno K., Zeigler M., Carmi R., Sokol J., Marxie D., O'Neill R.Y., van Diggelen O.P., Elleder M., Patterson M.C., Brady R.O., Vanier M.T., Pentchev P.G., Tagle D.A., "Niemann-Pick CI disease gene: homology to mediators of cholesterol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Watari H., Blanchette-Mackie E.J., Dwyer N.K., Glick J.M., Patel S., Neufeld E.B., Brady R.O., Pentchev P.G., Strauss J.F. III; "Niemann-Pick Cl protein: obligatory roles for N-terminal domains and lysosomal targeting in cholesterol mobilization."; Proc. Natl. Acad. Sci. U.S.A. 96:805-810(1999).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=98299797; PubMed=9634529; Greer W.L., Riddell D.C., Gillan T.L., Girouard G.S., Sparrow S.M., Byers D.M., Dobson M.J., Neumann P.E.; "The Nova Scotia (type D) form of Niemann-Pick disease is caused by G33097---T transversion in NPCI.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "The genomic organization and polymorphism analysis of the human Niemann-Pick Cl gene.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
MEDLINE=21623216; PubMed=11754101;
MEDLINE=21623216; PubMed=11754101;
Bauer C., Knoblich R., Bauer C., Finckh U., Hufen A., Kropp J.,
Braun S., Kustermann-Kuhn B. B., Schmidt D., Harzer K., Rolfs A.;
"NPC1: Complete genomic sequence, mutation analysis, and characterization of haplotypes.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=99355599; PubMed=10425213;
Morris J.A., Zhang D., Coleman K.G., Nagle J., Pentchev P.G.,
Carstea E.D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Niemann-Pick Cl gene.";
Biochem. Biophys. Res. Commun. 261:493-498(1999)
                                                                                                                                                                                                                                                                                                                                                                                                            HUMAN STANKALL.
NPC1 HUMAN STANKALL.
O15118; Q9P130;
30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 43, Last amnotation update)
...v-2004 (Rel. 43, Last amnotation update)
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VARIANTS NPC1,
Neumann P.
           Ohno K.;
                      .uminal
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33 TAPCSRGSSWSADLDKCMDCA-SCRARPHSDFCLGCAAAPPAPFRLLWPILG-TRANSMEM TRANSMEM TRANSMEM TRANSMEM TRANSMEM TRANSMEM TRANSMEM TRANSMEM TRANSMEM TRANSMEM CARBOHYD Query Match TRANSMEN DOMAIN Genew; EMBL; CHAIN EMBL; EMBL; EMBL; Matches 88 8888 ð MEDLINE=99452593; PubMed=10521297;
Millat G., Marcais C., Rafi M.A., Yamamoto T., Morris J.A.,
Pentchev P.G., Ohno K., Wenger D.A., Vanier M.T.;
"Niemann-Pick Cl disease: the 11061T substitution is a frequent mutant
allele in patients of Western European descent and correlates with a
classic juvenile phenotype."; Yamamoto T., Nanba E., Ninomiya H., Higaki K., Taniguchi M., Zhang H., Akaboshi S., Watanabe Y., Takeshima T., Inui K., Okada S., Tanaka A., Sakuragawa N., Millat G., Vanier M.T., Morris J.A., Pentchev P.G., type D (NPD) [MIM:257250]; also known as Niemann-Pick disease without sphingomyellinase deficiency, or Nova Soctian type. Because of evidence from biochemical changes, lack of complementation, and linkage mapping to the same chromosome site, NPD and NPC1 are MEDLINE=21313105; PubMed=11333381; Millat G., Marcais C., Tomasetto C., Chikh K., Fensom A.H., Harzer K., Wenger D.A., Ohno K., Vanier M.T.; Minemann-Pick CI disease: correlations between NPCI mutations, levels of NPCI procesin, and phenotypes emphasize the functional significance of the putative sterol-sensing domain and of the cysteine-rich MEDLINE=21313111, PubMed=11349231, Sun X., Marks D.L., Park W.D., Wheatley C.L., Puri V., O'Brien J.F., Kraft D.L., Lundquist P.A., Patterson M.C., Pagano R.E., Snow K.; Minemann-Pick C variant detection by altered sphingolipid trafficking and correlation with mutations within a specific domain of NPC1."; type C1 (NPC1) [MIM:257220]. NPC1 is an autosomal recessive lipid storage disorder, which affects particularly the brain, liver and spleen, and which is characterized by lysosomal accumulation of low density lipoprotein derived cholesterol. Clinical features include variable hepatosplenomegaly and severe progressive include variable hepatosplenomegaly and severe progressive. The age of onset can vary from infancy to late adulthood. DISEASE: Defects in NPC1 are the cause of Niemann-Pick disease endosomes and lysosomes. -!- DOWAIN: A cysteine-rich N-terminal domain and a C-terminal domain Mutations in NPC1 highlight a conserved NPC1-specific cysteine-rich "NPC1 gene mutations in Japanese patients with Niemann-Pick disease type C."; containing a di-leucine motif necessary for lysosomal targeting are critical for mobilization of cholesterol from lysosomes. PTM: Glycosylated. DISEASE: Defects in NPC1 are the cause of Niemann-Pick disease type C1 (NPC1) [MIM:257220]. NPC1 is an autosomal recessive lip Greer W.L., Dobson M.J., Girouard G.S., Byers D.M., Riddell D.C., Neumann P.E.; Ribeiro I., Marcao A., Amaral O., Sa Miranda M.C., Vanier M.T., Millat G.; AND VARIANTS ARG-215; VAL-858 AND GLN-1266 VARIANTS NPC1 ALA-378; MET-950; ARG-992 AND THR-1061. VARIANTS NPC1 TYR-177; CYS-978 AND VAL-1035. J. Hum. Genet. 65:1321-1329(1999). J. Hum. Genet. 68:1373-1385(2001). J. Hum. Genet. 68:1361-1372(2001). Am. J. Hum. Genet. 65:1252-1260(1999) [9] VARIANTS NPC1 GLN-958 AND ALA-1007. MEDLINE=99408226; PubMed=10480349; MEDLINE=21372069; PubMed=11479732; fum. Genet. 105:10-16(1999). VARIANT NPC1 THR-1061. loop.

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                                                                                                                                                  use by non-profit institutions as long as its content is in no way additied and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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N-LINKED (GLCNAC. . .) (POTENTIAL).
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PROSITE; PS50156; SSD; 1.
Signal; Glycoprotein; Transmembrane; Lysosome; Polymorphism; Disease mutation. 1 22 POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 72; DB 1; Length 1278;
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G0:0005764; C:lysosome; TAS.
G0:0005624; C:membrane fraction; TAS.
G0:000548; F:introllular transporter activity; TAS.
G0:0015248; F:sterol transporter activity; TAS.
G0:0016888; F:transmembrane receptor activity; TAS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8; Mismatches 17; IndelB
                    SIMILARITY: Belongs to the patched family. SIMILARITY: Contains 1 sterol-sensing (SSD) domain.
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considered to be allelic disorders.
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                                                                                                                                                                                                                                                                                                                                                                                      JOINED.
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EMBL; AF123046; AAF28875.1; -.
EMBL; AF123045; AAF28875.1; JOINED.
                                                                                                                                                                                                                                                                                                 AAD48006.1; JOINED
                                                                                                                                                                                                                                                                                                                                                                    JOINED
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InterPro; IPR003392; Patched.
InterPro; IPR000731; SSD 5TM.
Pfam; PF02460; Patched; I.
                                                                                                                                                                                                                                                            EMBL; AF002020; AAB63982.1; -.
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EGF-LIKE 40, CALCIUM-BINDI
EGF-LIKE 3.
BGF-LIKE 4, CALCIUM-BINDING.
BGF-LIKE 5, CALCIUM-BINDING.
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       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch)
       ---PPPPPAP----WTILGLDAMYVIM 272
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STRAIN-CD-1; TISSUE=Kidney;

Ota K., Kumar A., Wada J., Liu Z., Kanwar Y.S.;

Submitted (APR-1995) to the EMBL/GenBank/DDBJ databases.

-! FUNCTION: Structural component of connective tissue microfibrils that binds calcium. Fibrillin-1-containing microfibrils provide long-term force bearing structural support.

-! FTW: Forms intermolecular disulfide bonds either with other fibrillin-1 molecules or with other components of the microfibrils (By similarity).

-! SIMILARITY: Contains 47 EGF-like domains.

-! SIMILARITY: Contains 7 TGF-beta binding protein (TGFBP) domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
MEDLINE=95130561; PubMed=7829516;
Yin W., Germiller J., Sanguineti C., Smiley E., Pangilinan T.,
Pereira L., Ramirez F., Bonadio J.;
"Primary structure and developmental expression of Fbn-1, the mouse fibrillin gene.";
                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                               Q61554; Q60826;
01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
FBN1 OR FBN1 OR FBN-1.
                                                                                                                                                                                                             PRT; 2871 AA
       ---GDCSIACGPKPG--
                                              87 SLTFVLGLL----SGFLVWRRCRRER 108
                                                                                          273 WITYMAFLLVFFGAFFAVW--CYRKR 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Biol, Chem. 270:1798-1806(1995).
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                                                                                                                                                                                                             STANDARD;
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    235 TAPCS---
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FBN1_MOUSE
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A Straubberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

A Itaubnerg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Altaubnerg R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A plokins R.F., Jordan H., Moore T., Mang J., Heiteh F.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Stapleton M., Soares M.B., Bonaldo M.F., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Bosak S.A., McEwan P.J., McKernan K.J., Mallek J.A., Gunaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

A Nilalon D.K., Muzny D.M., Sodergren B.J., Iu X., Gibbs R.A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Buffard G.G.,

Rakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Rutterfield Y.S.N., Krzywinski M.I., Salaka U., Sanilus D.E.,

A Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                          "The DNA sequence and comparative analysis of human chromosome 20."; Nature 414:865-871(2001)
                                                                                                                    Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo
                                                                                                                                                    SEQUENCE FROM N.A.
TISSUE=Liver cancer;
Cheng Z., Gao G., Peng Y., Ren S., Chen Z., Han Z.;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                  10-0CT-2003 (Rel. 42, Created)
10-0CT-2003 (Rel. 42, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
C200RF155.
                                                    301 AA
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MEDLINE=22388257; PubMed=12477932;
    2100 PTEPDEAFRQICPFGSGII 2118
                                                   STANDARD;
                                                                                                              Homo sapiens (Human)
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                                                                                                                                     NCBI_TaxID=9606;
                                                    CTF5 HUMAN
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Pred. No. 46;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CHAIN
 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                      66 RNHCSGAGKAAPRPAAGAGAAAEAPGGQWGPASTPSLYENPWIIPNMLSMTRIGLAPVLG 125
                                                                                                                                                                                                                                                                                                                                                                                                                 83
                                                                                                                                                                                                                                                                                                                                                                   GLWLALLRSVAGEQAPGTAPCSRGSSWS--ADLDKCMDCAS--CRARP-----H 60
                                                                                                                                                                                                                                                                                                                                                                                          GSWGA-IRGAA--WAPGTRPSKRRACWALLPPVPCCLGCLAERWRLRPAALGIRLPGIGQ:65
'Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                  ---FRLLW------PILG
                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16-OCT-2001 (Rel. 40, Last sequence update)
15-WAR-2004 (Rel. 43, Last annotation update)
EGF-containing fibulin-like extracellular matrix protein 2 precursor (Fibulin-4) (Fibul-4) (Mutant p53 binding protein 1).
EFEMP2 OR FBLN4 OR MBP1.
                                 similarity)
         and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
-!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity)
-!- SIMILARITY: Belongs to the CDP-alcohol phosphatidyltransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gallagher W.M., Argentini M., Sierra V., Bracco L., Debussche L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'MBP1: a novel mutant p53-specific protein partner with oncogenic
                                                                                                                                                                                                                                                                                                                                            68;
                                                                                                                                                                                                                                                                                                                     Score 70; DB 1; Length 301; Pred. No. 8.9;
                                                                                                                                                                                                                                                                                                                                             42; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=FVB/N; IISSUE=Mammary gland;
MEDLINE=22388257; PubMed=12477932;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
                                                                                                                                                                                                                                                                                                301 AA; 32593 MW; 15CD406D29D3C405 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              GALSLIFVLGLLSGFLVWRRCRRERSS 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    126 YLIIEEDFNIALGVFALAGLTDLLDGFIA-RNWANQRSA 163
                                                                                                                                                                                                  PRIDATE PROTOCOLOGY CONTEST.

InterPro, IPR000462, CDP-OH P trans.

Pfam; PF01066; CDP-OH P transf; 1.

PROSITE; PS00379; CDP_ALCOHOL P TRANSF; FALSE_NEG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           443 AA
                                                                                                                                                                                                                                                                                                                                           13; Mismatches
                                                                                                                                                                                                                                                                           POTENTIAL.
                                                                                                                                                                                                                                                               POTENTIAL
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MEDLINE=99308589; PubMed=10380882;
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                                                                                                                                                                    EMBL; AF241784; AAG44472.1; -. EMBL; AL035461; CAB55278.1; -.
                                                                                                                                                                                           EMBL; BC015333; AAH15333.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (Rel. 40, Created)
(Rel. 40, Last seq
                                                                                                                                                                                                                                                                                                                     11.5%;
22.6%;
                                                                                                                                                                                                                                                     Transferase; Transmembrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Oncogene 18:3608-3616(1999)
                                                                                                                                                                                                                                                                                                                                            36; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus (Mouse)
                                                        class-I family.
                                                                                                                                                                                                                                                                                                                                 Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=10090;
                                                                                                                                                                                                                                                               179
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16-OCT-2001
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SEQUENCE
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Alterent R. D., Collise F. D., Sement C. P., Schmaner C. P., Schmaner C. P., Schmaner C. P., States C. P., States
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us-10-062-599-59.rsp

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65 ---- LGCAA 69
                                                                                                                                                                                                                                                                                                                                        443
515
558 AA;
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        26;
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                                                                                                 CARBOHYD
                                                                                                                                                                                                                                              CONFLICT
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                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
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DROME
          쉽
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                                                                                                                                                                                                 61
                                                                                                                                                                                                                                         12 LLIWAFLLLLGAASPÓDPEEPDSYTECTDGYEWDADSQHCRDVNECLTIPEACKGEMKC 71
                                                                                                                                                                                            13 LVLGLWLALLRSVAGEQAP----GTAPCSRGSSWSADLDKCMDCASCRARPHS-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A., AND SEQUENCE OF 83-112; 196-207 AND 422-443.

STRAIN=New England Deaconess Hospital;

MEDLINE=94267529; PubMed=8207484;

Litwack E.D., Stipp C.S., Kumbasar A., Lander A.D.;

Meuronal expression of glypican, a cell-surface
glycosylphosphatidylinositol-anchored heparan sulfate proteoglycan, in the adult rat nervous system.",
J. Neurosci. 14:3713-3724(1994).

I. FUNCTION: Cell surface proteoglycan that bears heparan sulfate.

May play an important role in the trophic and injury responses of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBL_TaxID=10116;
                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor. TISSUE SPECIFICITY: Nervous system.
PTM: This cell-associated glypican is further processed to give rise to a medium-released species.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A., AND SEQUENCE OF 24-55 AND 424-445.

ILSSSUB-BRAIDIN;
MEDLINE=93038690; PubMed=1417860;
Karthikeyan L., Maurel P., Rauch U., Margolis R.K., Margolis R.U.;
Karthikeyan L., Maurel P., Rauch U., Margolis R.K., margolis R.U.;
Karthikeyan L., Maurel P., Rauch U., Margolis R.K., margolis R.U.;
Holoning of a major heparan sulfate proteoglycan from brain and identification as the rat form of glypican.";
Biochem. Biophys. Res. Commun. 1888:385-401(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; L02896; AAA86439.1; -.
BMBL; L34067; AAA41251.1; -.
PIR; 156545; 156545.
InterPro; IPR001024; Fz domain.
InterPro; IPR001863; Glypican.
Pfam; PF001153; Glypican.
PROSITE; PS01207; GLYPICAN; 1.
PROSITE; PS01207; GLYPICAN; 1.
Proteoglycan; Heparan Bulfate; Glycoprotein; Signal; GPI-anchor;
Extracellular matrix; Lipoprotein.
N-LINKED (GLCNAC. . .) (POTENTIAL)
N-LINKED (GLCNAC. . .) (POTENTIAL)
                                                                                                                                                 26;
                                                                                               Score 70; DB 1; Length 443;
Pred. No. 13;
                                                                                                                                               33; Indels
                                -binked (GLCNAC. . .) (Po. 4969C0328A23DD88 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SIMILARITY: Belongs to the glypican family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Glypican-1 precursor (HSPG M12).
                                                                                                                                                                                                                                                                                                                                                                                                                                                              558 AA
                                                                                                                                               5; Mismatches
                                                                                                                                                                                                                                                                                         -----DFCLGCAAA------PPAP 74
                                                                                                                                                                                                                                                                                                                                        72 INHYGGYLCLPRSAAVISDLHGEGPPPP 99
                                               49425 MW;
                                                                                               11.5%;
ilarity 27.3%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rattus norvegicus (Rat).
  198 1
394 3
443 AA;
                                                                                               Query Match
Best Local Similarity
Matches 24; Conserv
                         CARBOHYD
SEQUENCE
                                                                                                                                                                                                                                                                                         62
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     CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME OF THE PROPERTY OF THE PR
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221 RSFVQGLGVASDVVRKVA--QVPLAPECSRA-----VMKLVYCAHCRGVPGARPCPDYC 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11 RLLVLGLWLA--LLRSVAGEQAPGTAPCSRGSSWSADLDKCMDCASCR----ARPHSDFC 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Stronach B.E., Renfranz P.J., Lilly B., Beckerle M.C.; "Muscle LIM proteins are associated with muscle sarcomeres and require dMEF2 for their expression during Drosophila myogenesis."; Mol. Biol. Cell 10:2329-2342(1999).
                                                                                                                                                                                      (POTENTIAL).
(POTENTIAL).
(POTENTIAL).
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MEDLINE=20196006; PubMed=10731132;
MEDLINE=20196006; PubMed=10731132;
Manarides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beaaley E.M.,
Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
                 GLYPICAN-1.
REMOVED IN MATURE FORM (FOTENTIAL).
GPI-anchor amidated serine (Potential).
                                                                                      N-LINKED (GLCNAC. ) (POTENTIAL).
N-LINKED (GLCNAC. ) (POTENTIAL).
O-LINKED (GLYCOSAMINOGLYCAN) (POTENTIAL).
O-LINKED (GLYCOSAMINOGLYCAN) (POTENTIAL).
O-LINKED (GLYCOSAMINOGLYCAN) (POTENTIAL).
                                                                                                                                                                                                                                                                             T -> A (IN REF. 2).
Y -> N (IN REF. 2).
A -> G (IN REF. 2).
I -> G (IN REF. 2; AA SEQUENCE).
B -> D (IN REF. 2; AA SEQUENCE).
1 -> T (IN REF. 2).
; E2878A854B9A1D7F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Muscle LIM protein Mip84B.
LIM3 OR MLP84B OR CG10699.
Drosophila melanogaster (Fruit fly).
Eukaryota, Metazoa, Arthropoda, Hexapoda; Insecta, Pterygota,
Boptera, Endopterrygota, Diptera, Brachycera; Muscomorpha;
Ephydroidea, Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 1; Length 558;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6; Mismatches 19; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Stronach B.E., Siegrist S.E., Beckerle M.C.; "Two muscle-specific LIM proteins in Drosophila."; J. Cell Biol. 134:1179-1195(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q24400; Q9VI62;
01-NOV-1997 (Rel. 35, Last sequence update)
15-MAR-2004 (Rel. 43, Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 70;
Pred. No. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=99326429; PubMed=10397768;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE #96387325; PubMed = 8794860;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     61734 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11.5%;
ilarity 37.7%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
443
515
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RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunk P.
Bodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunk P.
Bodson K., Doup L.E., Davagelista C.C., Ferraz C., Ferriera S., Fleischmann W., Glodek A., Gong F., Gorrell J.H., Gul Z., Galan P., Harris M.,
Allodek A., Gong F., Gorrell J.H., Gul Z., Galan P., Harris M.,
RA Harris N., Harris M., Howland T.J., Wei M.-H., Ibegwam C.,
Bad Alali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchm K.A.,
R. Kimmel B.E., Kodira C.D., Kraft C., Kraitz S., Kulp D., Lai Z.,
Lasko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,
R. Martell B.E., McIncosh T.C., McLocod M.P., Wepherson D.,
R. Martell B.E., McIncosh T.C., McLocod M.P., McDenson D.,
R. Merkello M., Pittman G.S., Pan S., Pollard J., Mushern D.E., Noshrefi A.,
R. Mount S.M., Mown Murphy B.M., Naskern D.R., Releat K., Remington K.S., Sunder R.P., Schel H., R.
R. Shue B.C., Sident Klamos I., Simpson M., Strong R., Sun B.,
R. Shue B.C., Sident Klamos I., Simpson M., Strong R., Sun B.,
Shie B.C., Sident Klamos I., Simpson M., Strong R., Sun B.,
R. Willams S.M., Woodage T., Worley K.C., Mu D., Yang S., Yao Q.A.,
R. Millams S.M., Woodage T., Worley K.C., Mu D., Yang S., Yao Q.A.,
R. Millams S.M., Woodage T., Worley K.C., Mu D., Yang S., Yao Q.A.,
R. A., Myers E.W., Rubin G.M., Venter J.C.;
C. Sidens S.M. Torong P.N., Zhong W., Zhou X., Zhu S., Zha A., Shar M., Shong G., Zha M., Shong G., Zha R., Shar S., Pollard J., Shar S., Shar M., Shar S., Shar M., Shong W., Strong W., Zhu S., Zha G., Shar S., Shar M., Shar S., Shar M., Shar S., Shar M., Shar S., Shar S., Shar M., Shar S., Shar

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SMART; SM00132; LIM; 5.
PROSITE; PS00478; LIM DOMAIN 1; 5.
PROSITE; PS50023; LIM DOMAIN 2; 5.
Nuclear protein; Repeat, LIM domain; Metal-binding; Zinc; Myogenesis; NUCLEAR LOCALIZATION SIGNAL (POTENTIAL). NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
 Developmental protein;
 Differentiation.

 DOMAIN
 12
 63
 LIM 1.

 DOMAIN
 65
 80
 GLY-RICH.

 DOMAIN
 120
 172
 LLM 2.

 DOMAIN
 175
 180
 NUCLEAR LOCAL.

 DOMAIN
 175
 180
 NUCLEAR LOCAL.

 DOMAIN
 222
 274
 LIM 2.

 DOMAIN
 222
 274
 LIM 3.

 DOMAIN
 225
 274
 LIM 3.

 DOMAIN
 325
 377
 LIM 4.
 EMBL; AF090832; AAC61591.1; -. EMBL; AE003672; AAF54063.1; -. HSSP; P32965; 1CTL. FlyBase; FBgn0014863; MlpB4B. InterPro; IRN001781; LIM. Pfam; PF00412; LIM; 5. ProDom; PD000094; LIM; 5. EMBL; X91245; CAA62627.1; -.

MEDLINE=22388257; PubMed=12477932; Strausberg R.L., Feingold B.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

Lung, Muscle, and Ovary;

SEQUENCE FROM N.A.

TISSUE=Colon,

Lehrach H., Reinhardt R., Yaspo M.-L.,
"The DNA sequence of human chromosome 21.";
Nature 405:311-319(2000).

110 AIARAPEGEGCPRCGGYVYAAEQMLARGRSWHKECFKCGTCKKGLDSILCCEAPDKNIYC 169 20 ALLRSVAGEQAP-----GTAPCSRGSSWSADLDKCMDCAS-----CRARPHSDFC 64 ABLINE=20209199; PubMed=10830953;
Hattori M., Fujiyama A., Taylor T.D., Watanabe H., Yada T.,
Hattori M., Fujiyama A., Taylor T.D., Watanabe H., Yada T.,
Hattori M., Fujiyama A., Taylor T.D., Watanabe H., Yada T.,
Soeda E., Ohki M., Takagi T., Sakaki Y., Taudien S., Blechschmidt K.,
Polley A., Menzel U., Delabar J., Kumpf K., Lehmann R., Patterson D.,
Reichwald K., Kump A., Schillhabel M., Schudy A., Zimmermann W.,
Rosenthal A., Kump J., Shillhabel M., Kawasaki K., Asakawa S.,
Shintani A., Sasaki T., Nagamine K., Mitsuyama S., Antonarakis S.E.,
Minoshima S., Shimizu N., Nordsiek G., Hornischer K., Brandt P.,
Ramser J., Beck A., Kages S., Hennig S., Riesselmann L., Dagand E.,
Wehrneyer S., Dorzym K., Gardiner K., Nizetic D., Francis F., 15; Gaps "Cloning of a novel human putative type Ia integral membrane protein mapping to 21q22.3."; Genomics 49:133-136(1998). Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo Pituitary tumor-transforming gene 1 protein-interacting protein (Pituitary tumor-transforming gene protein binding factor) (PTTG-binding factor) (PBP) (PTTG-PTTGIIP OR C210RPI OR C210RFI). CHARACTERIZATION, AND INTERACTION WITH PTTG1 Chien W., Pei L.,
"A novel binding factor facilitates nuclear translocation and
transcriptional activation function of the pituitary
trunor-transforming gene product.",
J. Biol. Chem. 275:19422-19427(2000). DB 1; Length 495; Yaspo M.-L., Aaltonen J., Horelli-Kuitunen N., Peltonen L., 7; Mismatches 37; Indels GLY-RICH. LIM 5. GLY-RICH. 2E559B9178E54C0E CRC64; P53801; Q9NS09; 01-0CT-1996 (Rel. 34, Created) 01-0CT-1996 (Rel. 34, Last sequence update) 01-0TAR-2004 (Rel. 43, Last annotation update) 180 AA 11.4%; Score 69.5; I 28.0%; Pred. No. 16; 170 KGCYAKKFGPKGYGYGQGGGAL 191 PRT; 65 LGCAAAPPAPFRLLWPILGGAL 86 SEQUENCE FROM N.A., CHARACTERIZATIOMEDLINE=20317150; PubMed=10781616; TISSUE=Thymus; MEDLINE=98234553; PubMed=9570958; 53525 MW; 23; Conservative STANDARD; Homo sapiens (Human) 379 3 421 4 475 4 495 AA; Query Match Best Local Similarity SEQUENCE FROM N.A. SEQUENCE FROM N.A. NCBI_TaxID=9606; HUMAN Lehrach H. DOMAIN DOMAIN DOMAIN SEQUENCE Matches SFFF HIDDELD DE LE DE L g à 유

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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@ibs-sib.ch).
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Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Didtchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Azabletchen M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Stapleton M.J., Ugdin T.B., Toshiyuki S., Carninci P., Prange C., Azaba S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.M., R. Villalon D.K., Muxny D.M., Sodergren E.J., Lu X., Gibbs R.A., R. Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., RA Bakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Ra Bakesley R.W., Touchman J.W., Schmutz J., Myers R.M., RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., R. Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.; Reneration and initial analysis of more than 15,000 full-length RT human and mouse cDNA sequences ")

Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)

-!- FUNCTION: May facilitate PTTG1 nuclear translocation.

-!- FUNCTION: May facilitate PTTG1.

-!- SUBGELULAR LOCATION: According to Ref.2, it is found in the mucleus. According to Ref.1, it is a type I membrane profes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                67 CAAAPPAP-----FRLIM-----PILGGALSLIFVLGLLSGFLVWRRCRRER 108
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19 FTPYWAREAGGG -> ARRTGGGASV (IN REF. 2).

14 TLLLGIA -> NPPEGHC (IN REF. 2).

20323 MW, FIE66014D49ECIDE CRC64;
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25.8%; Pred. No. 6.9;
tive 19; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              membrane protein.
TISSUE SPECIFICITY: Ubiquitous.
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EMBL, AL163300; CAB90552.1; --
EMBL, BC000415; AAH10415.1; --
EMBL, BC012858; AAH12858.1; --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL, BC019295, AAH19295.1; --
EMBL, BC020983, AAH30983.1; --
EMBL, BC031097, AAH31097.1; --
EMBL, BC031250, AAH31250.1; --
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180 AA;
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Search completed: March 1, 2004, 16:43:01 Job time : 19 secs

us-10-062-599-59.rspt

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March 1, 2004, 16:40:19; Search time 40 Seconds (without alignments) 899.227 Million cell updates/sec
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Copyright (c) 1993 - 2004 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

			Description	Q80xx9 rattus norv	Q9bzg3 homo sapien	Q9bzg2 homo sapien	0943g8 oryza sativ	Q82n80 streptomyce	Q9n0b3 macaca fasc	Q42839 hordeum vul	Q8vd70 mus musculu	Q8bmi5 mus musculu	Q80ya8 mus musculu	Q8z5r3 salmonella	Q81zx4 streptomyce	Q9qee6 indian citr	07u2q8 mycobacteri	053668 mycobacteri	018288 caenorhabdi
SUMMARIES			an T	Q80XX9	Q9BZG3	Q9BZG2	Q943G8	Q82N80	Q9N0B3	042839	Q8VD70	QBBMIS	Q80YA8	Q8Z5R3	Q812X4	O9OEE6	Q7U2G8	053668	018288
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			Match Length DB ID	129	333	426	019	377	341	332	387	219	1208	245	732	222	436	449	635
	æ	Query	Match	74.5	14.3	14.3	13.7	13.1	13.0	12.9	12.9	12.7	12.7	12.6	12.6	12.4	12.4	12.4	12.4
			Score	453	87	87	83.5	79.5	79	78.5	78.5	77.5	77.5	76.5	76.5	75.5	75.5	75.5	75.5
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17 75 12.3 370 4 096780 0957819 0069810 0069781 0069810 0069781	Q96kn9 homo sapien Q8cxg1 oceanobacil Q80mp4 indian citr Q860w5 mus musculu Q9a9x4 caulobacter P90890 caenorhabdi Q81243 streptomyce Q9p2p7 homo sapien O04393 homo sapien Q9BLNG cyprinus ca Q9BCAN homo sapien Q9BLNG corynebacte Q9nqQ2 homo sapien Q9nqQ2 homo sapien Q9nqQ2 homo sapien Q9nqQ2 homo sapien Q9nx99 homo sapien Q9nx99 homo sapien Q9xx9 aloligenes Q9y288 homo sapien Q9xx9 aloligenes Q9y288 homo sapien Q9xx9 aloligenes Q9xx9 aloligenes Q9xx9 aloligenes Q9xx9 aloligenes Q9xx9 aloligenes Q9xx9 blomo sapien Q9xx9 careptomyce Q9xx9 blomo sapien Q8s8 careptomyce Q9xx9 brown sapien Q8xx9 creeptomyce Q9xx9 brown sapien Q8xx9 creeptomyce Q7wx57 bordetella Q7wx50 bordetella	Created) Last sequence update) Last sequence update) Last annotation update) 1 FN14. 1; Craniata; Vertebrata; Buteleostomi; 1; Sciurognathi; Muridae; Murinae; Rattus. EMBL/GenBank/DDBJ databases.	Pane	
11 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	296KN9 080XG1 080MP4 080MP4 080MP5 2860MS 0963V4 094393 0963P7 098TH8 09	भेषेष्ट ≥ः	Score 45 Score 46 Pred. No. Misma MLLRSVAGI	TILGGALSI TILGGALSI TILGGALSI
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                                                                                                                                                                                                                                                                               Yousef G.M., Diamandis M., Jung K., Diamandis E.P.;
"Molecular cloning of a novel human acid phosphatase gene (ACPT) that is highly expressed in the testis.";
Genomics 74:385-395 (2001).
BMBL, AF3121918; AAK09396.1; -.
HSSP; P15309; 2HPA.
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"Molecular cloning of a novel human acid phosphatase gene (ACPT) that
is highly expressed in the testis.",
Genemics 74:385-395(2001).
EMBL, AF321918; AAX(9393.1; -...
HSSP; PIS309; 24PA.
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                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14.3%; Score 87; DB 4; Length 333; 35.3%; Pred. No. 0.49; tive 6; Mismatches 35; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     35; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                   GO, GO:0003993; F:acid phosphatase activity; IEA. InterPro; IPR000560; HisAc_phsphtse.
Pfam; PF00328; acid phosphat; 1.
PROSITE; PS00616; HIS ACID PHOSPHAT 1; 1.
PROSITE; PS00778; HIS ACID PHOSPHAT 2; 1.
SRQUENCE 333 AA; 35402 MW; OC0237096567B30F CRC64;
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GO; GO:0003993; F:acid phosphatase activity; IEA.

InterPro; IPR000566; HisAc phephtse.
Pfam; PF00328; acid phosphat; 1.

PROSITE; PS00616; HIS ACID PHOSPHAT 1; 1.

PROSITE; PS00778; HIS_ACID_PHOSPHAT_2; 1.

SEQUENCE 426 AA; 46089 MW; BE930398041DB061 CRC64;
(TrEMBLrel. 17, Created)
(TrEMBLrel. 17, Last sequence update)
(TrEMBLrel. 24, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             88 LTFVLGLLSGFLVWR-RCRRERSSP 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            308 VLVALSLGLGLLAWRPGCLRALGGP 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
MEDLINE=21309073; PubMed=11414767;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=21309073; PubMed=11414767;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-JUN-2001 (TrEMBLrel. 17, 01-JUN-2003 (TrEMBLrel. 24,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-JUN-2001 (TrEMBLrel. 17,
                                                                      Acid phosphatase variant 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (Human)
                                                                                                                     Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Acid phosphatase.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
    01-JUN-2001
01-JUN-2001
                                                01-JUN-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
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Q9BZG2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT
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ID O9
    à
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31 PG-TAPCSRGSSWSADLDKCMDCASCRARPHSDFCLGC--AAAPPAPFRLLWPILGGALS 87

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4;
351 PGCPAPCPLGRFYQL-----TAPARPPAHGVSCHGPYEAAIPPAP---VVPLLAGAVA 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           143 --NVPASPPPPRISLSPPPPSTPTQSGASSGSKSSNNGTVVAVGVAVAAVVVLGLAAGL 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ------6ASCRARPHSDF 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   64 CLGCAAAPPAPFRLLWP---------ILGGALSLTFVLGLLSG- 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           84 SPGDSSYTGGSSTSATVTASTDADPNAGDAVPTSAGDAIPSSACRKPAAARCPNRPATD-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      57; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KINASES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gramene, Q943G8; -.
Gramene, Q943G8; -.
GO; G0:0005524; F:ATP binding; IEA.
GO; G0:0004672; F:procein scrinc/threonine kinase activity; IEA.
GO; G0:0004672; F:procein activity; IEA.
GO; G0:0016740; F:transferase activity; IEA.
GO; GO:000468; P:protein amino acid phosphorylation; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPRO(0715) Prot kinase.
InterPro; IPRO(0715) Prot kinase.
InterPro; IPRO(0715) Fort kinase.
Pfam; PRO(059, pkinase; Ihr_pkin_AS.
Probom; PDO(0001; Prot Kinase; I.
PROSITE; PSO(107; PROTEIN KINASE ATP; I.
PROSITE; PSO(107; PROTEIN KINASE DOM; I.
PROSITE; PSO(108; PROTEIN KINASE TY; I.
ATP-binding; Kinase; Receptor; Serine/threonine-protein kinase; Transferase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 24.6%; Pred. No. 2;
Matches 34; Conservative 12; Mismatches 35; Indels 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            clone:P0046E05.";
submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
-!- EIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN
EMBL; AP003237; BAB67905.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=cv. Nipponbare;
Sasaki T., Matsumoto T., Yamamoto K.;
"Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 610 AA; 64405 MW; 2A7B3EBE83FA9303 CRC64;
                                                                                                                                                                                                                                                                                                                     01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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Last annotation update)
                                                                                                                                                                                                                                                                     610 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30 APGTAPCSRGSSWSADLDKCMD-------
                                                                              88 LIFVLGLLSGFLVWR-RCRRERSSP 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Created)
                                                                                                                                 401 VLVALSLGLGLLAWRPGCLRALGGP
                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                 Putative receptor protein kinase.
P0046E05.12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              98 --FLVWRRCRRERSSPPP 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             201 IYFFVSKRRRRRQHPPPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (TrEMBLrel. 24, (TrEMBLrel. 24, (TrEMBLrel. 25,
                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Oryza sativa (Rice)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=4530;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-JUN-2003
01-JUN-2003
01-OCT-2003
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Q82N80
ID Q82N8
AC Q82N6
DT 01-JT
DT 01-OC
DE HYPO1
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PRT;
                                                                                                                                       PROSITE; PS00407; CONNEXINS_1; 1.
PROSITE; PS00408; CONNEXINS_2; 1.
Gap junction; Transmembrane.
SEQUENCE 341 AA; 36784 MW 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; L34211; AAAS6787.1; -.
PIR; T04484; T04484.
HSSP; P23951; 2BAA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (TrEMBLrel. 01, (TrEMBLrel. 25,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-NOV-1996 (TrEMBLrel. 01,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           aleurone-specific expressi
Plant J. 6:579-589(1994).
                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SMART; SM00270; ChtBD1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chitinase (EC 3.2.1.14)
                                                                                                                               SMART; SM00037; CNX; 1
                                                                                                                                                                                                                                                               Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=4513;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-NOV-1996
01-OCT-2003
                                                                                                                                                                                                                                                                               29;
                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q42839
                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 libraries.";
Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: ONE GAP JUNCTION CONSISTS OF A CLUSTER OF CLOSELY PACKED
PAIRS OF TRANSMEMBRANE CHANNELS, THE CONNEXONS, THROUGH WHICH
MATERIALS OF LOW MW DIFFUSE FROM ONE CELL TO A NEIGHBORING CELL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     자.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15 LGLWLALLRSVAGEQAPGTAPCSRGSSWSADLDKCMDCASCRARPHSDFCLGCAAAPPAP
                                                                                                                                                                                                                                                                                                                                                                    Ikeda H., Ishikawa J., Hanamoto A., Shinose M., Kikuchi H., Shiba T., Sakaki Y., Hattori M., Omura S., "Complete genome sequence and comparative analysis of the industrial microorganism Streptomyces avermitilis.";

Nat. Biotechnol. 21:526-531(2003).

EMBL, AP005026; BAC69133.1;

Interpro, IPR007016; Way C.

Pfam; PF04932; Way C: 1.

Hypothetical protein; Complete proteome.

SEQUENCE 377 AA; 36860 MW; 7964B23DFE6F29AA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SIMILARITY).
-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO THE CONNEXIN FAMILY.
EMBL; ABG46017; BAB01299.11; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Osada N., Hida M., Kusuda J., Tanuma R., Iseki K., Hirai M., Terao Suzuki Y., Sugano S., Hashimoto K.;
"Isolation of full-length cDNA clones from macaque brain cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Unnamed protein product (Gap junction protein) (Connexin).
Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
Bukaryota, Metazoa, Chordata, Craniata; Vertebrata; Buteleostomi;
Cercopithecinae; Macaca.
NCBL TaxID=9541;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -! - SUBUNIT: A CONNEXON IS COMPOSED OF A HEXAMER OF CONNEXINS (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13;
                                                                                                                    STRAIN=MA-4680 / ATCC 31267 / NCIMB 12804 / NRRL 8165;
MEDLINE=21477403; PubMed=11572948;
Omura S., Ikeda H., Ishikawa J., Hanamoto A., Takahashi C.,
Shinose M., Takahashi Y., Horikawa H., Nakazawa H., Osonoe T.,
Kikuchi H., Shiba T., Sakaki Y., Hattori M.;
"Genome sequence of an industrial microorganism Streptomyces
avermitilis: deducing the ability of producing secondary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 16; Length 377;
                             Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
NCBI_TaxID=33903;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indela
                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
STRAIN=MA-4680 / ATCC 31267 / NCIMB 12804 / NRRL 8165;
                                                                                                                                                                                                                                                         metabolites.";
Proc. Natl. Acad. Sci. U.S.A. 98:12215-12220(2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 79.5; Di
Pred. No. 3.3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         158 SRLALRILAAAITVTAAALGSLTGF 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  75 FRLLWPILGGALSLT-FVLGLLSGF 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                    MEDLINE=22608306; PubMed=12692562;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13.1%;
34.1%;
           Streptomyces avermitilis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     29; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 29; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (BY SIMILARITY
                                                                                                      FROM N.A.
                                                                                                    SEQUENCE
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Q9N0B3 RESULT 6 09N0B3

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---RPPCTGVVDCY 158
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R GO; GO:000884; F:endochitinase activity; IEA.

R GO; GO:0016798; F:ndochitinase activity; IEA.

R GO; GO:0016798; F:hdycolase activity; IEA.

R GO; GO:0016598; F:carbohydrate metabolism; IEA.

R GO; GO:0016998; P:call wall catabolism; IEA.

R GO; GO:000613; P:caltin catabolism; IEA.

R InterPro; IPR001002; Chitin binding 1.

R InterPro; IPR00187; Chitin binding 1.

R Pfam; PR00187; Chitin bind 1.

R Pfam; PR00181; CHTINBIRDMC

R PRINTS; PR00451; CHTINBIRDMC

R ProDom; PD000609; Chitin binding 1; 1.

R ProDom; PD000609; Chitin binding 1; 1.

R ProDom; PD000609; Chitin binding 1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9 LIRLLVLGLWIALLRSVAGEQAPGTAPCSRGSSWSADLDKCMDCASCRARPHSDFCLGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hordeum vulgare (Barley).
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
Triticeae; Hordeum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE=Seed,
MEDLINE=95078949; PubMed=7987416;
Leah R., Skriver K., Knudsen S., Ruud-Hansen J., Raikhel N.V.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'Identification of an enhancer/silencer sequence directing the leurone-specific expression of a barley chitinase gene.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13.0%; Score 79; DB 6; Length 341; 27.9%; Pred. No. 3.4; tive 9; Mismatches 46; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        69 AAPPAPFRLIMPILGGALSLIFVLGLLSGFLVWRRCRRERSSPP 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       341 AA; 36784 MW; 4A71DEA938F0FA0C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chitin-binding, Glycosidase, Hydrolase.
SEQUENCE 332 AA; 35369 MW; 1B38554F49AC9E0F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Last sequence update)
Last annotation update)
GO; GO:0005922; C:connexon complex; IEA.
GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0015285; F:connexon channel activity; IEA.
GO; GO:0007154; P:cell communication; IEA.
InterPro; IPR0005050; Connexin.
Pfam; PF00029; connexin.
PRINTS; PR00206; CONNEXIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            332 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             119 LLRTLLEAAFGALNYLLFGFLAPNKFPCT-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE, PS00773; CHITINASE 19 1; 1. PROSITE; PS00774; CHITINASE 19 2; 1. PROSITE; PS00026; CHITIN BINDING; 1.
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ACCOUNT TO THE PROPERTY OF THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 셤
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ----QA 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18 GSTARVLQPLFLPLLLLLLLGGQGGGGGGGGGGCDCASESQKRYGPFCCRGCPKGHYMKA 77
                                                                                                                                                                13 LVLGLWLALLRSV----AGEQAPG-TAP----CSRGSSWSADLDKCMDCASCRARPHSDF 63
                                                                                                                                                                                                                                      13 IVLSAALAMAMVVRAQQCGSQAGGATCPNCLCCSRFGYCGSTSDYC--GAGCQSQ----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -----SRGSSWSADLDKCMDC-----ASCRARP----HS
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                                                                                      23; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Musinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-UNN-2003 (TrEMBLrel. 24, Last annotation update)
Similar to tumor necrosis factor receptor superfamily, member 12.
TNFRSF2S OR TNFRSF12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           85;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12.9%; Score 78.5; DB 11; Length 387; 18.9%; Pred. No. 4.3;
        Score 78.5; DB 10; Length 332;
Pred. No. 3.7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE=Salivary gland;
Strausberg R.;
Submitted (VO-2001) to the EMBL/GenBank/DDBJ databases.
Submitted (VO-2001) to the EMBL/GenBank/DDBJ databases.
Submitted (VO-2001) to the EMBL/GenBank/DDBJ databases.
SMBJ; BC017526; AAH17526.1; -.
RGJ; GC01004872; Fireeptor activity; IEA.
GG; GC10004872; Fireeptor activity; IEA.
GG; GC10007165; Prisqual transduction; IEA.
InterPro; IPR006189; Death.
InterPro; IPR006189; Death.
R InterPro; IPR001389; TNFR_C6.
R Pfam; PF00531; death; 1.
R Pfam; PF00051; DBATH; 1.
R SMART; SM00005; DBATH; 1.
R SMART; SM00005; DBATH; 1.
R PROSITE; PS50017; DBATH DOMAIN; 1.
R PROSITE; PS00652; TNFR_NGFR_1; 1.
R PROSITE; PS00652; TNFR_NGFR_1; 1.
R PROSITE; PS00652; TNFR_NGFR_2; 1.
                                                                                  38; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                64 CLGCAAAPPAPFRLLWPILGGALSLTFVLGLLSGFLVWR-RCR 105
                                                                                                                                                                                                                                                                                                                                                                                              66 CSGCGPTPPGPSP-----GGGVSSIISRDLFEQFLLHRDRCQ 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Receptor.
SEQUENCE 387 AA; 41640 MW; F16644666BAD68D3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               387 AA
                                                                              9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4 GSLRRILRILVLGLWLALLRSVAGE-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
ch 12.9%;
l Similarity 32.0%;
33; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           35; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PGTAPC----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best_Local Similarity
Matches 35; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WRRCR 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WOPCK 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     101
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
        Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               08VD70
                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 9
Q8BMI5
ID Q8BM1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q8VD70
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219 AA.

PRT;

PRELIMINARY;

QBBMIS

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The FANTOM Consortium,

The RIKEN Genome Exploration Research Group Phase I & II Team;

The RIKEN Genome Exploration Research Group Phase I & II Team;

The RIKEN Genome Exploration Research Group Phase I & II Team;

The RIKEN Genome Exploration Research Group Phase I & II Team;

The RIKEN Genome Exploration Research Group Phase I & II Team;

RIK TO Genome Exploration Research Group Phase I & II Team;

The RIKEN Genome Exploration Research Group Phase I & II Team;

The RIKEN Genome Exploration Research Research Group Phase I & II Team;

The RIKEN FOR THE RESEARCH R
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99 LAGLRCQSLDKPCEASPCLNGGTCRVASGIFEC----TCSAGFSGQFCEVVKTLPLPLPF 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19 LALLIRSVAGEQAPGTAPCSRGSSW--SADLDKCMDCASCRARPHSDFCLGCAAAP-PAPF 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
STRAIN-C57BL/6; TISSUE=Brain;
STRAIN-C57BL/6; TISSUE=Brain;
Straubberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Straubberg R.L., Zeeberg B., Wagner L., Shemmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetchow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haish F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleron M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                       Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                <u>ئ</u>
01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Weakly similar to neurogenic locus notch 3 protein (Fragment).
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12.7%; Score 77.5; DB 11; Length 219; 30.0%; Pred. No. 3.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        76 RLLWPILGGALS -- LTFVLGLLSGFLVWRRCRRERSSPPP 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (TrEMBLrel. 24, Last sequence update) (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                45;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30; Conservative 16; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-JUN-2003 (TrEMBLrel. 24, Created)
                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
STRAIN-C57BL/6J; TISSUE=Forelimb;
MEDLINE=22354683; PubMed=12466851;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5930402A21 protein (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=10090;
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01-OCT-2003
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1088 LAGLRCQSLDKPCEASPCINGGTCRVASGIFEC---TCSAGFSGOFCEVVKTLPLPLPF 1143
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Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Kulyk S.W., Vilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., Mniting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S., Krzywinski M.I., Skalaka U., Smailus D.E., Schnerch A., Schein J.B., Jones S.J., Marra M.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=CT18;
MEDLINE=21534947; PubMed=11677608;
Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             19 LALLRSVAGEQAPGTAPCSRGSSW--SADLDKCMDCASCRARPHSDFCLGCAAAP-PAPF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales,
Enterobacteriaceae, Salmonella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9;
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                                                                                                                                                                                                                                             Strausberg R., Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                        EMBL; BC043114; AAH43114.1; -

GO; GO:0005509; F:calcium ion binding; IEA.

GO; GO:0005199; F:calcium ion binding; IEA.

GO; GO:0005199; F:calcium ion binding; IEA.

InterPro; IPR00152; Asx hydroxyl_S.

InterPro; IPR00152; Asx hydroxyl_S.

InterPro; IPR001881; EGF_Ca.

InterPro; IPR001881; EGF_II.

InterPro; IPR006209; EGF_II.

R InterPro; IPR006209; EGF_II.

R InterPro; IPR005209; Laminin_G.

Pfam; PF00008; EGF, 13.

R PRIMTS; PR00101; EGFLAMININ.

R PRIMTS; PR00118; EGF, 15.

R SWART; SM00179; EGF_CA; 13.

R SWART; SM00179; EGF_CA; 13.
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01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Flagellar biosynthetic protein Flip.
STY218 OR FLIP OR T0898.
Salmonella typhi.
                                                                                                                                                                                 Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12.7%; Score 77.5; Di
30.0%; Pred. No. 16;
Live 16; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             245 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE; PS00010; ASX HYDROXYL; 8. PROSITE; PS00022; EGF 1: 14. PROSITE; PS01186; EGF 2; 9. PROSITE; PS00125; LAM G_DOMAIN; 2.
                                                                                                                                                                                             [2]
SEQUENCE FROM N.A.
STRAIN=C57BL/6; TISSUE=Brain;
                                                                                                                                                              and mouse cDNA sequences."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 30; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
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                                                                                                                                                                                        SEQUENCE FROM N.A.
STRAIN=TY2 / ATCC 700931;
MEDLINE=22531367; PubMed=12644504;
Deng W., Liou S.-R., Plunkett G. III, Mayhew G.F., Rose D.J.,
Burland V., Kodoyianni V., Schwartz D.C., Blattner F.R.;
"Comparative genomics of Salmonella enterica serovar Typhi strains Ty2
and CT18.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6 LRRILLRILVLGLWLALLRSVAGEQAPG--TAP-CSRGSSWSADLDKCMDCASCRARP---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MRRILFLSLAGIW--LFSPAAAAQLPGLISQPLAGGGQSWSLSVQTLVFITSLTFLPAIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebaihia M.
           Baker S., Basham D., Brooks K., Chillingworth T., Connerton P., Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J., Feltwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagels K., Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C., Quail M., Rutherford K., Simmonds M., Skelton J., Stevens K., Mhitchead S., Barrell B.G.;

"Complete genome sequence of a multiple drug resistant Salmonella enterica servovar Typhi CT18.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       27;
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STRAIN=MA-4680 / ATCC 31267 / NCIMB 12804 / NRRL 8165;
MEDLINE=21477403; PubMed=11572948;
Omura S., Ikeda H., Ishikawa J., Hanamoto A., Takahashi C.,
Shinose M., Takahashi Y., Horikawa H., Nakazawa H., Osonoe T.,
Kikuchi H., Shiba T., Sakaki Y., Hattori M.;
"Genome sequence of an industrial microorganism Streptomyces avermitiis: deducing the ability of producing secondary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
12.6%; Score 76.5; DB 16; Length 245;
Best Local Similarity 30.8%; Pred. No. 4.5;
Matches 33; Conservative 9; Mismatches 38; Indels 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       59 LMMTSFTRIIIVFGLLRNALGTPSAPPNQV-----LLGLALFLTFFI 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Streptomyces avermitilis.
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      60 --HSDF------CLGCAAAPPAPFRLLWPILGGALSLTFVL 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C9B9931F0653A4D4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Proc. Natl. Acad. Sci. U.S.A. 98:12215-12220(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Streptomycineae, Streptomycetaceae, Streptomyces.
NCBI_TaxID=33903;
                                                                                                                                                                                                                                                                                                                                  J. Bacteriol. 185:2330-2337(2003).

EMBL; AL627272; CAD05727.1; --
EMBL; AE016837; AA068576.1; --
GO; GO:0019861; C:flagellum; IEA.
GO; GO:0016020; C:membrane; IEA.
GO; GO:0009306; P:protein secretion; IEA.
InterPro; IPR005838; TypeIII_P.
Pfam; PF00813; Flip;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Putative serine/threonine protein kinase. PKN16 OR SAV4717.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRINTS; PRO1302; TYPE3IMPPROT.
ProDom; PD002566; TYPEIII P; 1.
TIGRPAMS; TIGRO1103; filp; 1.
PROSITE; PS01060; FILP 1; 1.
PROSITE; PS01060; FILP 1; 1.
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SEQUENCE 245 AA; 26755 MW;
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InterPro, IPR008891; Viral NABP.
Pfam; PF05515; Viral NABP; I.
SEQUENCE 222 AA; 25455 MW; 636A47058DD8D01D CRC64;
                                          Query Match
Best Local Similarity 35.44
Best Local Si Conservative
                                                                                                                                                                                                                                                                                                                                                                                                Mycobacterium bovis.
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nes 35; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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Matches
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   SOR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GSKATGMAQCAYAPHRLYCTRPGVLAAAVDPADGKVLMSRGDAKRHSDGTVRPPVLSGGL 455
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               46 LDKCMDCASCRARPHSDFC----LGCAAAPPAPFRLLW--------PILGGAL 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Nucleotide sequence, genome organization and phylogenetical analysis of Indian citrus ringspot virus.";
Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF84962; AAR01314.1. ...
                                       Ikeda H., Ishikawa J., Hanamoto A., Shinose M., Kikuchi H., Shiba T.,
Jakaki Y., Hattori M., Omura S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                         "Complete genome sequence and comparative analysis of the industrial microorganism Streptomyces avermitilis."; Nat. Biotechnol. 21:526-531(2003).
                                                                                                Mat. Biotechnol. 21:556-531 (2003)

R Mat. Biotechnol. 21:556-531 (2003)

R GO; GO:0005624; F:ATP binding; IEA.

GO; GO:0004674; F:protein-tyrosine kinase activity; IEA.

GO; GO:00046713; F:protein-tyrosine kinase activity; IEA.

GO; GO:00046113; F:protein-tyrosine kinase activity; IEA.

GO; GO:00064618; P:protein-tyrosine kinase activity; IEA.

GO; GO:0006468; P:protein amino acid phosphorylation; IEA.

InterPro; IPR002372; Bac_PQ_repeat.

R InterPro; IPR002372; Bac_PQ_repeat.

R InterPro; IPR002290; Ser_thr_pkinase.

R InterPro; IPR002290; Ser_thr_pkinase.

R InterPro; IPR002290; Ser_thr_pkinase.

R Pfam; PF000069; pkinase; 1.

R Pfam; PF00101; Pcot_kinase; 1.

R ProDom; PD000001; Prot_kinase; 1.

R SMART; SM00220; STKC; 1.

R SMART; SM00220; TYRKC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Indian citrus ringspot virus: a proposed new species with some affinities to potex-, carla-, fovea- and allexiviruses."; Arch. Virol. 145:1895-1908(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               T.WAY-2000 (TrEMBLrel. 13, Created)
01-WAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
23-XDa protein (Putative 23 kDa nucleic acid binding protein).
Indian citrus ringspot virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 16; Length 732;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=20496665; PubMed=11043949;
Rustici G., Accotto G.P., Noris E., Masenga V., Luisoni E.,
Milne R.G.;
                                                                                                                                                                                                                                                                                                                                                                             PROSITE; PS00107; PROTEIN KINASE ATP; 1.
PROSITE; PS50011; PROTEIN KINASE DOM; 1.
PROSITE; PS00108; PROTEIN KINASE ST; 1.
Kinase; Serine/Hoconine-protein Kinase; Complete proteome.
SEQUENCE 732 AA; 76174 MW; 41E6556B3D5EA722 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12.6%; Score 76.5; DB 16; Length 29.2%; Pred. No. 13; Live 12; Mismatches 36; Indels
              STRAIN=MA-4680 / ATCC 31267 / NCIMB 12804 / NRRL 8165;
MEDLINE=22608306; PubMed=12692562;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Viruses; ssRNA positive-strand viruses, no DNA stage
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 29.29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           202 ALPHR--IVPRVHAAPGLHKLVYVGWTAIRTNGWYRRYLLVQVLFGSVVLGSSFHSIRVA 259
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                                                                                                                                                                                21 RGSQIRSVRLLP---WRPFTRFPV---CPSGTSPYSRGTHSQPSYVRCONCERAROWFRA 74
                                                                                                                            3 RGSLRRLLRLLVLGLWLALLRSVAGEQAP-GTAPCSRGSSWSADLDKCMDCASCRA--RP
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                                                                19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 436;
      Length 222;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Putative membrane protein.
RV0246 OR MT0260 OR MTV034.12.
Mycobacterium tuberculosis.
Bacteria, Actinobacteria, Actinobacteridae; Actinomycetales; Corynebacterinee; Mycobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           436 AA; 45353 MW; 1A2AB43B1052F07B CRC64;
                                                                                                                                                                                                                                                                                                         75 HDGPRCLHQRPDYSRLQAPPDPFQHLNSFEPILLAALSV 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-OCT-2003 (TrEMBLrel. 25, Created)
01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Probable conserved integral membrane protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Corynebacterineae, Mycobacteriacaae, Mycobacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12.4%; Score 75.5; DB 16; ilarity 23.0%; Pred. No. 9.9; Conservative 16; Mismatches 52;
12.4%; Score 75.5; DB 12; 35.4%; Pred. No. 5.2; tive 7; Mismatches 38;
                                                                                                                                                                                                                                                   60 H-SDFCL-----GCAAAPPAPFRLL---WPILGGALSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -----ALSLIFVLGLLSGFLVWRRCR 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     260 AVPGDQPDEVVAVVLFVCVGLLGGIALWNRVR 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   436 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           449 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     57 ARPHSDFCLGCAAAPPAPFRLLW----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; BX248334; CAD93116.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-JUN-1998 (TrEMBLrel. 06, 01-MAR-2002 (TrEMBLrel. 20, 01-OCT-2003 (TrEMBLrel. 25,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
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NUEL TaxID=1773;

RP SEQUENCE FROM N.A.

RC STRAINE=98295987;

RA GOLGON S.V., Elglmeier K., Farkhill J., Garnier T., Churcher C., Harris D., RA GORGON S.V., Elglmeier K., Gas S., Barry C.E. III, Tekaia F., Andrew D. B. Cohllingworth T., Connor R., Baccock K., Basham D. Brown D. Chillingworth T., Connor R., Baccock K., Boborne J., Rahlin N., Holroyd S., Roris R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S., Ranistor S., Seeger K., Skelton S., Squares S., Squares R., Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;

RA Buston J.E., Taylor K., Whitehead S., Barrell B.G.;

RT Complete genome sequence...;

RT Complete Genome sequence...;

RE SEQUENCE FROM N.A.

RC STRAIN=CDC 1551 / Gohkosh;

RA SIGNATE STON J., Alland D., Eisen J.A., Ermolace M., Salzberg S.L., RA Fleischmann R.D., Alland D., Eisen J.A., Ermolace M., Salzberg S.L., RA Clonay J.F., Nelson W.C., Umayam L.A., Ermolace M., Salzberg S.L., RA Bishai W.;

RA Clonay J.F., Nelson W.C., Umayam L.A., Ermolace M., Salzberg S.L., RA Bishai W.;

RA Bishai W.;

RY Hole Genome comparison of Mycobacterium tuberculosis clinical and Laboratory strains...;

RY Hole Genome comparison of Mycobacterium tuberculosis clinical and Laboratory strains...;

RE MEM: ALOS1929; CAA17338.1; ALT_INIT.

RY HOLSE MEM: ALOS6934; AAK44478.1; -.

RY TUGR; MTO260; -.

RY TUGR; MTO260; -.

RY Complete proteome.

RY Complete proteome.

RY Complete proteome.

RY Complete proteome.
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57 ARPHSDFCLGCAAAPPAPFRLLW-

9 9 à

Search completed: March 1, 2004, 16:43:54 Job time: 42 secs

----- BILGG----- 84

1 MARGSLRRLLRLLVLGLWIALLRSVAGEQA--PGTAPCSRGSS--WSADLDKCMDCASCR

12.4%; Score 75.5; DB 16; Length 449; 23.0%; Pred. No. 10; tive 16; Mismatches 52; Indels 49

35; Conservative

Matches

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Query Match Best Local Similarity 49; Gaps

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February 11, 2004, 10:32:18; Search time 40 Seconds (without alignments) 452.371 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1. /SLIDSIJ/gogdata/geneseqy_embl/AA1981.DAT;*
1. /SLIDSIJ/gogdata/geneseqy_embl/AA1982.DAT;*
1. /SLIDSIJ/gogdata/geneseqy_embl/AA1982.DAT;*
1. /SLIDSIJ/gogdata/geneseqy_embl/AA1983.DAT;*
1. /SLIDSIJ/gogdata/geneseqy_embl/AA1986.DAT;*
1. /SLIDSIJ/gogdata/geneseqy_embl/AA1986.DAT;*
1. /SLIDSIJ/gogdata/geneseqy_embl/AA1987.DAT;*
1. /SLIDSIJ/gogdata/geneseqy_embl/AA1980.DAT;*
1. /SLIDSIJ/gogdata/geneseqy_embl/AA1980.DAT;*
1. /SLIDSIJ/gogdata/geneseqy_embl/AA1980.DAT;*
1. /SLIDSIJ/gogdata/geneseqy_embl/AA1990.DAT;*
1. /SLIDSIJ/gogdata/geneseqy_embl/AA1992.DAT;*
1. /SLIDSIJ/gogdata/geneseqy_embl/AA1992.DAT;*
1. /SLIDSIJ/gogdata/geneseqy_embl/AA1992.DAT;*
1. /SLIDSIJ/gogdata/geneseqy_embl/AA1992.DAT;*
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1. /SLIDSIJ/gogdata/geneseqy_embl/AA1992.DAT;*
1. /SLIDSIJ/gogdata/geneseqy_embl/AA1999.DAT;*
1. /SLIDSIJ/gogdata/geneseqy_embl/AA1999.DAT;*
1. /SLIDSIJ/gogdata/geneseqy_embl/AA1999.DAT;*
1. /SLIDSIJ/gogdata/geneseqy_embl/AA1999.DAT;*
1. /SLIDSIJ/gogdata/geneseqy_embl/AA1999.DAT;*
1. /SLIDSIJ/gogdata/geneseqy_embl/AA1999.DAT;*
2. /SLIDSIJ/gogdata/geneseqy_embl/AA2000.DAT;*
2. /SLIDSIJ/gogdata/geneseqy_embl/AA2001.DAT;*
2. /SLIDSIJ/gogdata/geneseqy_embl/AA2001.DAT;*
2. /SLIDSIJ/gogdata/geneseqy_embl/AA2001.DAT;*
2. /SLIDSIJ/gogdata/geneseqy_embl/AA2001.DAT;*
                                                                                                                                                                                                                                                                                                                                                                                                      1 MARGSLRRLLRLLVLGLWLA......LSGFLVWRRCRRERSSPPPX 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Geneseq 19Jun03:*
/SIDS1/gcgdata/geneseq/geneseqp-embl/AA1980.
GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /SIDS1/gcgdata/geneseq/genesegp-embl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1107863 segs, 158726573 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       seq length: 0
seq length: 2000000000
                                                                                                                                                                                                                                                                                                                                         US-10-062-599-59
                                Copyright
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115:
117:
119:
220:
221:
23:
                                                                                                                                                                                                                                                                                                                                      Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Scoring table:
                                                                                                                                OM protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Minimum DB
Maximum DB
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                                                                                                                                                                                                                                                                                                                                                                                                             Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Database
                                                                                                                                                                                                 Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	Human secreted pro	Human liver clone	Human transmembran	Human TWEAK recept	Human NF-kB activa	Human type 1 trans	Lung cancer-associ	Mouse type 1 trans	Himan TWRAK recent
SUMMARIES	AAW73409	AAW88506	AAY57940	AAU03498	ABP61512	AAU79827	ABU56716	AAU79828	AAT103500
DB	202	20	21	22	23	23	24	23	22
Length	114	129	129	129	129	129	129	129	309
* Query Match	99.8	93.9	93.9	93.9	93.9	93.9	93.9	74.0	71.2
% Query Score Match Length DB II	607	571	571	571	571	571	571	450	433
Result No.	н	7	e	4	2	9	7	89	σ

Cyre Learness newill	secreted		BAFF rece	BAFF		BAFF	Human BAFF recepto	Ä	- 4	ď	ą.	2	~	Ď	Human JST576 BAFF	IJ						യ	2B10 AMH-receptor.	Human protein sequ	cancer-	Novel human diagno	_	Full length mouse	Canine mature Flt-	Canine Flt-3 ligan	Human protein SEQ	secrete		Novel human protei	
ABV01463	19	AAY91552	AAE22269	AAE22266	AAE22267	AAE22270	AAE22271	AAE22268	AAE22242	ABP70117	ABP70118	ABB81483	AAE35227	ABP97721	AAE22243	ABG32546	ABG32542	ABG23348	ABG32541	AAU75788	AAU09880	AAB01337	AAR80631	AAB95174	ABR01798	ABG26293	AAY56750	AAY54990	AAY58208	AAY58207	AAM79666	ABJ10913	ABP60987	ABP60986	AAM24485
2,1	12	21	23	23	23	23	23	23	23	23	23	23	24	24	23	23	23	22	23	23	23	21	16	22	24	22	21	21	21	21	22	23	23	23	22
112	155	156	185	185	185	185	185	185	185	1388	1388	184	184	184	566	333	375	426	426	426	426	426	508	224	224	152	448	448	250	276	141	356	326	370	234
4.5		'n.	S		'n,	'n	•	4.	٠	4	4.	14.3	4.	4.	4.	•	4.	4.	4		•												12.3		
4	274.5	4	4	'n.	ď	ij	ï.	9	8	88.5	ω.	87	87	87	87	87	87	87	87	87	87	80.5	ö	79	79	77	77	77	76.5		92	75	75	75	74
0	11	12	13	14	15	16	17		19	20	21	22	23	24	25	56	27	28	59	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

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Secreted protein, human, protein therapy; gene therapy; blood disorder; pathological condition; diagnosis; cancer; neurological disorder; developmental abnormality; foetal deficiency; leukaemia; hepatic disease; immune system disorder; Alzheimer's disease; cognitive disorder; schlzophrenia; prostate disease; autoimmune disorder; AIDS.
                                                                                                                                                                                                                                   /note= "unspecified amino acid"
                                                                                           Human secreted protein encoded by Gene No. 13
                                                                                                                                                                                                         Location/Qualifiers
114
                       AAW73409 standard; Protein; 114 AA
                                                                                                                                                                                                                                                                                                                             97US-0056296.
97US-0044039.
97US-0048093.
97US-0048101.
                                                                                                                                                                                                                                                                                                         98WO-US10868
                                                                    (first entry)
                                                                                                                                                                                                             Key
Misc-difference
                                                                                                                                                                                                                                                                                                                             29-AUG-1997;
30-MAY-1997;
30-MAY-1997;
30-MAY-1997;
                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                          WO9854206-A1
                                                                                                                                                                                                                                                                                                         28-MAY-1998;
                                                                    19-FEB-1999
                                                                                                                                                                                                                                                                                03-DEC-1998.
RESULT 1
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                                                                                                                                                                                                                                                                                                                                                                              The DNA sequences of the invention and their corresponding secreted polypeptides are useful for preventing, treating or ameliorating medical conditions, e.g. by protein or gene therapy. Also pathological conditions can be diagnosed by determining the amount of the new polypeptides in a sample or by determining the presence of mutations in the DNA sequences. Specific uses are described for each of the DNA sequences of proteins, based on which tissues they are most highly expressed in, and include developing products for the diagnosis or treatment of cancer, tumours, neurological disorders, leukaemias, diseases of the immune system (including allergies or asthma), hepatic disease, Alzheimer's and cognitive disorders, schizophrenia, prostate diseases, alzheimer's and disorders and AIDS. The polypeptides are also useful for identifying their binding partners.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9
                                                                                                                                                                                                                                                                                                                    This sequence is encoded by a cDNA of the invention, designated Gene No. 13. This sequence represents a human secreted protein, and is expressed in keratinocytes and to a lesser extent in endothelial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MARGSLRRLLRLLVLGLWLALLRSVAGEQAPGTAPCSRGSSWSADLDKCMDCASCRARPH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MARGSLRRLLRLLVLGLWLALLRSVAGEQAPGTAPCSRGSSWSADLDKCMDCASCRARPH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                        New isolated human genes - useful for diagnosis and treatment of, e.g. cancers, neurological disorders, immune diseases, developmental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SDFCLGCAAAPPAPFILLWPILGGALSLTFVLGLLSGFLVWRRCRRERSSPPP 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SDFCLGCAAAPPAPFRLLWPILGGALSLTFVLGLLSGFLVWRRCRRERSSPPP 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 20; Length 114; 6.5e-56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Indels
                                                                                                                             Ni J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human liver clone HP10432-encoded membrane protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protein; HP10432; human; liver.
                                                                                                                             Feng P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Prea. ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99.8%; Score 607;
                                                                                                                             Endress GA,
                                                                                                                                                                                                                                                                                      Claim 11; Page 153; 188pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAW88506 standard; Protein; 129 AA
               97US-0048356.
97US-0050935.
97US-0056250.
                                                                                                                                                                                                                                                       disorders or blood disorders
                                                                                             (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             98WO-JP02445
97US-0048190
                                                             97US-0056293
                                                                                                                                         Yu G;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches 113; Conservative
                                                                                                                           Dillon PJ,
                                                                                                                                           Ruben SM,
                                                                                                                                                                          WPI; 1999-070209/06.
                                                                                                                                                                                                                                                                                                                                                                    cells and placenta.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            114 AA;
                                                                                                                                                                                        N-PSDB; AAV08823.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Transmembrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO9855508-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           03-JUN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30-MAR-1999
                                                             29-AUG-1997
                              30-MAY-1997
29-AUG-1997
                                                                                                                                            Rosen CA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAW88506;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                           Carter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 2
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1 MARGSLRRLLRLLVLGLWLALLRSVAGEQAPGTAPCSRGSSWSADLDKCMDCASCRARPH 60
                                                                                                                                                                                                                                                                                             This is the amino acid sequence of a transmembrane protein encoded by human liver cDNA clone HP10432 (see AAV84374). The encoded protein has a signal-like N-terminal region and one internal transmembrane domain. The invention provides nucleotide sequences (see AAV84359-76) coding for 18 transmembrane proteins (see AAW88491-508), vectors containing such polynucleotides, and eukaryotic cells containing the vectors. The proteins can be used as antigens or as compositions in the preparation of antibodies against the proteins. The polynucleotides can be used as probes for gene diagnosis, and as gene sources for gene therapy and large-scale production of proteins encoded by the cDNA. The host cells are used for the detection of ligands corresponding to the expressed proteins, and the screening of low mol.wt. medicines.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MARGSLRRILRLLVLGLWLALLRSVAGEQAPGTAPCSRGSSWSADLDKCMDCASCRARPH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; transmembrane protein; HTWPN; diagnosis; immunospecific; antipoliferative; neuroprotective; immune disorder; reproductive disorder; mosch muscle disorder; neurological disorder; gastrointestinal disorder; developmental disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SDFCLGCAAAPPAPFRLLWPILGGALSLTFVLGLLSGFLVWRRCRREKFTTP 113
                                                                                                                                                                                         New human proteins containing transmembrane domains and their encoding sequences - useful in the preparation of antibodies and large-scale protein production, gene diagnosis, and gene therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SDFCLGCAAAPPAPFRLLWPILGGALSLTFVLGLLSGFLVWRRCRRERSSPPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 571; DB 20; Length 129;
Pred. No. 4.4e-52;
0; Mismatches 6; Indels C
                                                                                                                                                                                                                                                                 Claim 1; Page 152-153; 178pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human transmembrane protein HTMPN-64.
                                                                                                      Yamaguchi T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAY57940 standard; Protein; 129
                                                (PROT-) PROTEGENE INC. (SAGA) SAGAMI CHEM RES CENTRE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 93.9%;
Best Local Similarity 94.7%;
Matches 107; Conservative C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       98US-0087260.
98US-0091674.
98US-0102954.
              97JP-0144948
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cell proliferative disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99WO-US11904
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23-MAR-2000 (first entry)
                                                                                                                                      WPI; 1999-045730/04.
                                                                                                    Sekine S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    129 AA;
                                                                                                                                                           N-PSDB; AAV84374
              03-JUN-1997;
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02-JUL-1998;
02-OCT-1998;
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                                                                                                    Kato S,
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Corley NC;

Guegler KJ, Corley N Kaser MR, Baughn MR;

Lal P, Hillman JL, Yue H, , Patterson C, Gorgone GA,

98US-0109869

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(INCY-) INCYTE PHARM INC
                    WPI; 2000-072605/06
24-NOV-1998;
               Au-Young J;
         Tang YT, 1
Bandman 0,
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AAZ56698 to AAZ56776 encode AAY57877 to AAY57955 which represent human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        transmembrane proteins designated HTMPN-1 to HTMPN-79, respectively. The transmembrane protein have immunospecific, antiproliferative and neuroprotective activities. The human transmembrane proteins, polynucleotides encoding them and other compositions and methods from the present invention, can be used for the diagnosis, treatment or prevention of immune, reproductive, smooth muscle, neurological, gastrointestinal, developmental and cell proliferative disorders. The HTMPN's can be used to treat or prevent disorders associated with a decreased expression or activity of HTMPN.
                                                                                            Proteins, polynucleotides, vectors, host cells and antibodies used to diagnose, treat or prevent immune, reproductive, smooth muscle, neurological, gastrointestinal, developmental and cell proliferative
                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; Page 163; 229pp; English.
N-PSDB; AAZ56761
                                                                                                                                                                                                                                                                         disorders
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129 AA; Sequence

1 MARGSLRRILBLLVLGLWLALLRSVAGEQAPGTAPCSRGSSWSADLDKCMDCASCRARPH 60 Length 129; 6; Indels Score 571; DB 21; Pred. No. 4.4e-52; 0; Mismatches 93.9%; Query Match Best Local Similarity 94.7 Matches 107; Conservative ð

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Gaps

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9

1 MARGSLRRLLRLLVLGLWLALLRSVAGEQAPGTAPCSRGSSWSADLDKCMDCASCRARPH

61 SDFCLGCAAAPPAPFRLLWPILGCALSLTFVLGLLSGFLVWRRCRRERSSPPP 113 SDFCLGCAAAPPAPFRLIMPILGGALSLTFVLGLISGFLVWRRCKRREKFTTP 113 19 ò

рp

AAU03498 standard; Protein; 129 AA AAU03498 RESULT

AAU03498;

Human TWEAK receptor (TWEAKR) polypeptide.

(first entry)

26-SEP-2001

joint; ocular neovascularisation, diabetic retinopathy, neovascular glaucoma, retinoblastoma, retinopathy of prematurity, retrolental fibroplasia, rubeosis, uveitis, macular degeneration, arthritis, rheumatism, corneal graft neovascularisation, psoriasis, metastatic condition, malignant tumour, sarcoma, carcinoma, benign tumour, haemophilic joint preneoplastic condition, myocardial anglogenesis, wound granulation, scleroderma, vascular adheshon, telangiactasis, ischaemia, human atherosclerotic plague neovascularisation, coronary atherosclerosis, IWEAK receptor; TWEAKR; tumour necrosis factor; TNF; angiogenesis; peripheral atherosclerosis

Homo sapiens

"Mature human TWEAKR protein" /note= "Signal peptide" Location/Qualifiers 28..129 /note= "! 1..78 Protein Peptide Domain

/note= "Extracellular domain" 79..101 /note= "Transmembrane domain" 'note= "Intracellular domain" 99US-0172878. 10-MAY-2000; 2000US-0203347. 19-DEC-2000; 2000WO-US34755 ..129 (IMMV) IMMUNEX CORP. WPI; 2001-417975/44. N-PSDB; AAS03963. WO200145730-A2 20-DEC-1999; 28-JUN-2001 Wiley SR; Domain Domain

Modulating angiogenesis in a mammal for treating diseases mediated by angiogenesis, e.g. solid tumours and vascular deficiencies of cardiac or peripheral tissue, by administering antagonist or agonist of TWEAK

Example 1; Fig 1; 46pp; English.

TWEAK protein is a member of the tumour necrosis factor (TNF) family and induces angiogenesis. TWEAKR may therefore be used to screen for and develop TWEAKR agonists into the modulation of angiogenesis, to be used in the treatment and diagnosis of human disease. The disorders mediated by angiogenesis include ocular disorders characterised by ocular neovascularisation such as diabetic retinopathy, neovascular glaucoma, retinoplastoma, retinopathy of prematurity, retrolental fibroplasia, rubeosis, uveitis, macular degeneration and corneal graft neovascularisation, and inflammatory diseases such as arthritis, rheumatism and psoriasis. Other treatable diseases include malignant and metastatic conditions such as sarcomas and carcinomas, The sequence represents the human TWEAK receptor (TWEAKR) protein. The benign tumours and preneoplastic conditions, myocardial angiogenesis, haemophilic joints, scleroderma, vascular adhesions, atherosclerotic plaque neovascularisation, telangiectasia, wound granulation, coronary atherosclerosis, peripheral atherosclerosis and ischaemia.

·: 9 9 1 MARGSLRRLLRLLVLGLWLALLRSVAGEQAPGTAPCSRGSSWSADLDKCMDCASCRARPH 1 MARGSLRRLLRLLVLGLWLALLRSVAGEQAPGTAPCSRGSSWSADLDKCMDCASCRARPH 0; Gaps Length 129; Indels 9 Score 571; DB 22; Pred. No. 4.4e-52; 0; Mismatches 6; 93.9%; Matches 107; Conservative Query Match Best Local Similarity

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61 SDFCLGCAAAPPAPFRLLWPILGGALSLTFVLGLLSGFLVWRRCRRREKFTTP 113 61 SDFCLGCAAAPPAPFRLLWPILGGALSLTFVLGLLSGFLVWRRCRRERSSPPP ABP61512 standard; Protein; 129 AA RESULT 5 ABP6151

113

Human NF-kB activating protein SEQ ID NO 178. (first entry) 30-SEP-2002

ABP61512;

Human; NF-kB; nuclear factor kappa B; mouse; antiinflammatory; immunomodulator; cytostatic; antiinfective; osteopathic; nootropic;

us-10-062-599-59.rag

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The invention relates to a purified protein (I), comprising one of 90 fully defined sequences (ABP61424-ABP61513) or a protein based on any of the sequences but with some amino acids deleted, substituted or added and with a NF-KB (nuclear factor Kappa B) activating effect. The protein and encoding gene (ABQ91912-ABQ92001) are useful in diagnosis and screening inhibitors or promoters to control excessive activation or inhibition and for treating e.g. inflammations, autoimmune diseases, cancers, inflammations, autoimmune diseases or ischaemic infections, bone diseases, AIDS, neurodegenerative diseases or ischaemic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    vulnerary; TWEAK agonist; Fn14 agonist, angiogenesis; tumour progression; tumour necrosis factor family; TNF family; TWEAK receptor; myocardial ischaemic condition; myocardial infarction; wound healing; burn healing; gastric ulcer; tissue transplantation; organ transplantation; neovascularisation; vascular insufficiency; cancer; inflammatory macular degeneration; diabetic retinopathy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MARGSLRRLLRLLVLGLWLALLRSVAGEQAPGTAPCSRGSSWSADLDKCMDCASCRARPH 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MARGSLRRLLRLLVLGLWLALLRSVAGEQAPGTAPCSRGSSWSADLDKCMDCASCRARPH 60
                                                                                                                                                                                                                                                                                                                                                                                                                             NF-approximatelykB activating gene and expressed protein, applicable diagnosis and screening inhibitors or promoters to control excessive activation or inhibition for treating e.g. inflammations, autoimmune
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neuroprotective; anti-HIV; autoimmune disease; cancer; infection; bone disease; AIDS; neurodegenerative disease; ischaemic disorder.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 571; DB 23; Length 129;
Pred. No. 4.4e-52;
0; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                  Nagano
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 4; Page 814-815; 841pp; Japanese.
                                                                                                                                                                                                                                                                                                                                  Muramatsu S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAU79827 standard; Protein; 129 AA
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                                                                                                                                                                                                              28-DEC-2000; 2000JP-0402288.
26-MAR-2001; 2001JP-0088912.
24-AUG-2001; 2001JP-0254018.
                                                                                                                                                                        25-DEC-2001; 2001WO-JP11389.
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Matches 107; Conservative
                                                                                                                                                                                                                                                                                                                                  A, Honda G,
                                                                                                                                                                                                                                                                                                                                                                    WPI; 2002-583617/62
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                                                                                               WO200253737-A1
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                                                          Homo sapiens
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The invention describes methods of modulating angiogenesis and inhibiting tumour progression using TWEAK (a novel member of the tumour necrosis factor or TWF family) receptor agonists. Conditions which can be treated using the agonists include myocardial ischaemic conditions (e.g. myocardial infarction), wound healing (e.g. burn healing and healing of gastric ulcers), and tissue and organ transplantations to promote neovascularisation, particularly in subjects suffering from vascular insufficiency (e.g. diabetic patients). Inhibition of angiogenesis and subsequently neovascularisation is useful in treatment of cancer, inflammatory macular degeneration and diabetic retinopathy. This sequence represents the human type I transmembrane protein Fn14, a TWEAK receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lung cancer-associated polypeptide; cytostatic; emphysema; atelectasis; antiinflammatory; antiasthmatic; non-small cell lung cancer; atelectasis; small cell lung cancer, benign lesion; precancerous lesion; bronchitis; chronic obstructive pulmonary disease; hypersensitivity pneumonitis; interstitial pulmonary fibrosis; fibrosis; asthma; bronchiectasis.
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                                                                                                                                                                                                                                                         Methods of modulating anglogenesis and inhibiting tumour progression,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           93.9%; Score 571; DB 23; Length 129; 94.7%; Pred. No. 4.4e-52;
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                                                                                                                                                                                         Zheng T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
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                                                                                                                                                                                         Jakubowski A,
                                                                                                                                                                                                                                                                                                             Disclosure; Fig 10A; 37pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABUS6716 standard; Protein; 129 AA.
                                                                                                                                                                                                                                                                             using TWEAK receptor agonists
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                                                                                                                    14-SEP-2000; 2000US-232355P
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                                                                                   12-SEP-2001; 2001WO-US28451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         described in the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches 107; Conservative
                                                                                                                                                                                                                          WPI; 2002-383103/41.
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Best Local Similarity
                                                                                                                                                      (BIOJ ) BIOGEN INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            129 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO200286443-A2.
              WO200222166-A2
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                                                 21-MAR-2002
                                                                                                                                                                                           Browning J,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
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cancer-associated polymucleotides and polypeptides are used for identifying a compound that modulates a lung cancer-associated polypeptide, for inhibiting proliferation of a lung cancer-associated polypeptide, for inhibiting proliferation of a lung cancer-associated lung cancer in a patient and for treating a mammal having lung cancer by administering a modulatory compound identified. The methods are useful for treating lung cancer, such as small cell lung cancer, non-small cell lung cancer, such as small cell lung cancer, nor other benign or precancerous lesions, e.g. atelectasis, emphysema, bronchitis, chronic obstructive pulmonary disease, fibrosis, hypersensitivity pneumonitis, interstitial aul monary disease, fibrosis, hypersensitivity pneumonitis, interstitial and polypeptides are useful for diagnostic purposes and as targets for screening for therapeutic compounds that modulate lung cancer, such as an antibodies. Sequences ABU56408-ABU5675 represent lung cancer-associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to a method for detecting a lung cancer-associated transcript in a cell from a patient, comprising contacting a biological sample from the patient with a polymucleotide that selectively hybridises to a sequence that is at least 80 % identical to a gene that exhibits increased or decreased expression in lung cancer samples. Lung
                                                                                                                                                                                                                                                                                                                   Detecting a lung cancer-associated transcript in a cell from a patient for treating lung cancer, by contacting a biological sample from the patient with a polynucleotide that exhibits increased or decreased
                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 27; Page 429; 453pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              polypeptides of the invention.
                                                                                                                                                  (EOSB-) EOS BIOTECHNOLOGY INC
10-MAY-2001; 2001US-290492P.
09-NOV-2001; 2001US-339245P.
13-NOV-2001; 2001US-350666P.
29-NOV-2001; 2001US-334370P.
12-APR-2002; 2002US-372246P.
                                                                                                                                                                                                                                                                                                                                                                                                expression in lung cancer
                                                                                                                                                                                                                                                 WPI; 2003-093161/08
                                                                                                                                                                                                Murray R;
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· 0 1 MARGSLRRILRILVLGLWLALLRSVAGEQAPGTAPCSRGSSWSADLDKCMDCASCRARPH 60 9 1 MARGSLRRLLRLLVLGLWLALLRSVAGEQAPGTAPCSRGSSWSADLDKCMDCASCRARPH Gaps . 0 Query Match 93.9%; Score 571; DB 24; Length 129; Best Local Similarity 94.7%; Pred. No. 4.4e-52; Matches 107; Conservative 0; Mismatches 6; Indels (8

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RESULT 8

AAU79828 standard; Protein; 129 AA AAU79828; AAU79828

(first entry) 15-JUL-2002

Mouse type 1 transmembrane protein Fn14.

tumour progression; Type 1 transmembrane protein Fn14; mouse; cytostatic; cardiant; vulnerary; TWEAK agonist; Fn14 agonist; angiogenesis; tumour progress tumour necrosis factor family; TNF family; TWEAK receptor; myocardial ischaemic condition; myocardial infarction; wound healing; burn healing; gastric ulcer; tissue transplantation; organ transplantation; necvascularisation; vascular insufficiency; cancer; inflammatory macular degeneration; diabetic retinopathy.

The invention describes methods of modulating angiogenesis and inhibiting tumour progression using TWEAK (a novel member of the tumour necrosis factor or TNR family) receptor agonists. Conditions which can be treated using the agonists include myocardial ischaemic conditions (e.g. myocardial infrarction), wound healing (e.g. burn healing and healing of agastric ulcers), and tissue and organ transplantations to promote neovascularisation, particularly in subjects suffering from vascular insufficiency (e.g. diabetic patients). Inhibition of angiogenesis and subsequently meavascularisation is useful in treatment of cancer, inflammatory macular degeneration and diabetic retinopathy. This sequence represents the mouse type 1 transmembrane protein Fn14, a TWEAK receptor modulating angiogenesis and inhibiting tumour progression, 0; SDPCLGCAAAPPAHFRLLWPILGGALSLVLVLVLALVSSFLVWRRCRRREKFTTP 61 SDFCLGCAAAPPAPFRLLWPILGGALSLTFVLGLLSGFLVWRRCRRERSSPPP Length 129; Indels / Match 74.0%; Score 450; DB 23; 1 Local Similarity 75.2%; Pred. No. 2.1e-39; nes 85; Conservative 6; Mismatches 22; Jakubowski A, Disclosure, Fig 10B; 37pp; English. using TWEAK receptor agonists 12-SEP-2001; 2001WO-US28451 14-SEP-2000; 2000US-232355P described in the invention. Burkly L, WPI; 2002-383103/41 BIOJ) BIOGEN INC 129 AA; WO200222166-A2 Mus musculus. Browning J, 21-MAR-2002 Methods of Seguence Query Match Best Loca Matches 셤 à g ö

1 MARGSLRRLLRLLVLGLWLALLRSVAGEQAPGTAPCSRGSSWSADLDKCMDCASCRARPH 60 Gaps

0

RESULT 9

AAU03500 standard; Protein; 309 AA AAU03500

AAU03500;

(first entry) 26-SEP-2001

TWEAK receptor; TWEAKR; tumour necrosis factor; TNF; angiogenesis; Human TWEAK receptor-Fc (TWEAKR-Fc) fusion polypeptide.

ocular neovascularisation; diabetic retinopathy; neovascular glaucoma; retinopathy of prematurity; retrolental fibroplasia; rubeosis; uveitis; macular degeneration; arthritis; rheumatism; corneal graft neovascularisation; psoriasis; metastatic condition; malignant tumour; sarcoma; carcinoma; benign tumour; haemophilic joint; preneoplastic condition; myocardial angiogenesis; wound granulation; scleroderma; vascular adhesion; telangiectasia; ischaemia; human; atherosclerotic plaque neovascularisation; coronary atherosclerotis peripheral atherosclerosis; human IgGl; TWEARR-FC; fusion protein.

Homo sapiens.

Synthetic. us-10-062-599-59.rag

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Modulating angiogenesis in a mammal for treating diseases mediated by angiogenesis, e.g. solid tumours and vascular deficiencies of cardiac or peripheral tissue, by administering antagonist or agonist of TWEAK
                                                          /note= "From TWEAKR extracellular domain. Specifically
referred to in Claims 4 and 10"
                                 'note= "Mature human TWEAKR-Fc fusion protein.
Specifically referred to in Claim 11"
                                                                                   "From a BglII cloning site"
                "Signal peptide"
Location/Qualifiers
                                                                                                  /note= "Fc portion"
                                                                                                                                                                                                                                                                                                  Claim 4; Page 45-46; 46pp; English.
                                                                                                                                                                            10-MAY-2000; 2000US-0203347.
                                                                                                                                                     19-DEC-2000; 2000WO-US34755
                                                                                                                                                                     99US-0172878
                                                                                   /note= "1
82..309
                         309
                 note=
                                                                            80..81
                                                                                                                                                                                             (IMMV ) IMMUNEX CORP.
                                                                                                                                                                                                                               2001-417975/44.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         309 AA;
                                                                                                                                                                                                                                      N-PSDB; AAS03965
                                                                                                                    WO200145730-A2
                                                                                                                                                                     20-DEC-1999;
                                                                                                                                    28-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                               Wiley SR;
                                                                                                                                                                                                                                                                                  receptor
                         Protein
        Peptide
                                                 Domain
                                                                                           Region
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The sequence represents a fusion protein consisting of the human TWEAK receptor (TWEAKE) protein extracellular domain fused to an Fc portion from human IgG1. This fusion protein, TWEAKEF, is used in the preparation of TWEAKE agonists and antagonists. The TWEAK protein is a member of the tumour necrosis factor (TNF) family and induces angiogenesis. TWEAKE may therefore be used to screen for and develop TWEAKE agonists for the modulation of angiogenesis, to be used in the treatment and diagnosis of human disease. The disorders mediated by angiogenesis include ocular disorders characterised by ocular neovascularisation such as diabetic retinopathy, neovascular glaucoma, retinopathy of prematurity, retrolental fibroplasia, rubecosis, uveitis, macular degeneration and corneal graft neovascularisation, and inflammatory diseases such as arthritis, rheumatism and psoriasis. Other treatable diseases include malignant and members and the conditions such as sarconas and carcinomas, benign tumours and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          preneoplastic conditions, myocardial angiogenesis, haemophilic joints, scleroderma, vascular adhesions, atherosclerotic plaque neovascularisation, telangiectasia, wound granulation, coronary atherosclerosis, peripheral atherosclerosis and ischaemia.
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1 MARGSLRRLLRLLVLGLWLALLRSVAGEQAPGTAPCSRGSSWSADLDKCMDCASCRARPH 60
                                                                                                                                                        1 MARGSLRRLLRLLVLGLWLALLRSVAGEQAPGTAPCSRGSSWSADLDKCMDCASCRARPH 60
                                                                                                                                                                                                              61 SDFCLGCAAAPPAPFRLLWPILGGALSLTFVLGLLSGFLVWRRCRRERSSPP 112
Score 433; DB 22; Length 309;
Pred. No. 3.2e-37;
2; Mismatches 5; Indels 2:
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1 Similarity 74.1%;
83; Conservative
  Query Match
Best Local Similarity
                                Best Loc
Matches
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22; Gaps

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Human, secreted protein, diagnosis, cytostatic, immunosuppressive, antiHIV, antiAflammatory; nootropic; neuroprotective, antiAllergic, osteopathic; antiArthritic, antiBacterial; antidiabetic; antiasthma; antipsoriatic; cardiant; gene therapy; cancer; neurological disorder; immune disease; inflammation; blood disorder; tumour; chromosome 16.
                                          Human secreted protein sequence encoded by gene 13 SEQ ID NO:136.
AAY91463 standard; Protein; 112 AA.
                                                                                                                                                          98US-0094657.
98US-0095486.
98US-0095454.
98US-0095455.
98US-0096319.
                                                                                                                                                                                                      (HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                              99WO-US17130
                            (first entry)
                                                                                                                 WO200006698-A1.
                                                                                                    Homo sapiens.
                                                                                                                                              29-JUL-1999;
                            29-JUN-2000
                                                                                                                                                                                 06-AUG-1998;
                                                                                                                                                                  05-AUG-1998;
                                                                                                                                10-FEB-2000
                                                                                                                                                           30-JUL-1998
                                                                                                                                                                          06-AUG-1998
             AAY91463;
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New isolated human genes and the secreted polypeptides they encode, useful for diagnosis and treatment of e.g. cancers, neurological disorders, immune diseases, inflammation or blood disorders

Shi Y;

Duan R, Moore PA, Young PE, Brewer

, Florence KA, Young PE, Brewe Ebner R, Olsen HS, Mucenski M;

GA, Rosen CA, Ruben SM, Wei Y, Ni J, Florence KA Endress GA, Ebner R, Ols

Komatsoulis GA,

Soppet DR,

Lafleur

2000-195282/17.

N-PSDB; AAA26358

Claim 11; Page 465; 634pp; English.

the polymetroclus sequences it will apply the human secreted proteins given in APV91451 to APV91651. The human secreted proteins given in APV91451 to APV91651. The human secreted proteins can have activities based on the tissues and cells they are artially antimidiammatory; nootropic; neuroprotective; antiallergic; osteopathic; antiarthritic; antibacterial; antidiabetic; antiallergic; osteopathic; antiarthritic; antibacterial; antidiabetic; antiallergic; osteopathic; antiarthritic; antibacterial; antidiabetic; corresponding secreted proteins are useful for preventing, treating or ameliorating medical conditions, e.g. by protein or gene therapy. Also pathological conditions can be diagnosed by determining the amount of the proteins in a sample or by determining the presence of mutations in the polymucleotides. Specific uses are described for each of the polymucleotides based on which tissues they are most highly expressed in, and include developing products for the diagnosis or treatment of cancer, tumours, neurodegenerative disorders, developmental abnormalities and foetal deficiencies, blood disorders, diseases of the immune system, autoimmune diseases, hepatic and renal disease, inflammation, allergies, allaheimer's and behavioural disorders, schizophrenia, cardiovascular disorders, aethmat, sepsis, acre, poorlassis, cardiovascular disorders aethma, sepsis, acre, poorlassis, cardiovascular disorders aethma, sepsis, acre, poorlassis, cardiovascular disorders aethmat, the proteins of polymucleotides can also be used as food additives or preventives. partners. The proteins are also useful for identifying their binding AAA26337 to AAA26345 and AAY91450 are sequences used in the exemplification of the present invention. The polynucleotide sequences given in AAA26346 to AAA26458

112 AA; Sequence

---WRSCDKTHTCPP 90

61 SDFCLGCAAAPPAPFRLL

cardiovascular disorders, reproductive disorders, gastrointestinal disorders, respiratory disorders and metabolic disorders. The proteins or polynucleotides can also be used as food additives or preservatives. The proteins are also useful for identifying their binding partners. AAAA6337 to AAA26345 and AAA2460 are sequences used in the exemplification of the present invention.

1;

Gaps

1;

0

1; Mismatches

54; Conservative

Matches

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Similarity

155 AA;

Sequence

8888888

Query Match Local

DB 21; Length 155;

45.1%; Score 274.5; DB 2 96.4%; Pred. No. 6.1e-21;

1 MARGSLRRLLRLLVLGLWLALLRSVAGEQAPGTAPCSRGSSWSADLDKCMDCA-SC 55 MARGSIRRILIRILVIGIMIALIRSVAGEQAPGTAPCSRGSSWSADIDKCMDCSTSC 56

Human secreted protein sequence encoded by gene 13 SEQ ID NO:225.

(first entry)

29-JUN-2000

AAY91552;

AAY91552 standard; Protein; 156 AA

RESULT 12

AAY91552

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ij
                                                                                                                                                Human; secreted protein; diagnosis; cytostatic; immunosuppressive; antilHIV; antinflammatory; nootropic; neuroprotective; antiallergic; osteopathic; antiarthritic; antibacterial; antidiabetic; antiarthrima; antipsoriatic; cardiant; gene therapy; cancer; neurological disorder; immune disease; inflammation; blood disorder; tumour; chromosome 16.
                             Gaps
                                                                                                                                  secreted protein sequence encoded by gene 13 SEQ ID NO:277.
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⊢
 21; Length 112;
                Indels
  .5;
.4.3e-21;
0;
DB
Score 274.5; I Fred. No. 4.3e-1; Mismatches
                                                                                    AAY91604 standard; Protein; 155 AA
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98US-0095486.
98US-0095454.
98US-0095455.
45.1%;
96.4%;
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                                                                                                                   (first entry)
               54; Conservative
        Similarity
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                                                                                                                                                                                                 Homo sapiens.
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Query Match
Best Local S:
Matches 54,
                                                                                                    AAY91604;
                                                                                                                                  Human
                                                                      RESULT 11
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human secreted proteins given in AAV91451 to AAV91691. The human secreted proteins can have activities based on the tissues and cells they are expressed in. Examples of the activities are: cytostatic. immunosuppressive; antiHIUV; antiHIIINT antiHIINT antiH
                                                                                                                                                                                                                                        Human, secreted protein, diagnosis, cytostatic, immunosuppressive, antiHIV, antiinflammatory; nootropic; neuroprotective, antiallergic; osteopathic; antiarthritic, antibacterial, antidiabetic; antiathritic, antibactery, ancerial, antidiabetic antiathma; antiporiatic; cardiant, plee therapy; cancer; neurological disorder; immune disease; inflammation; blood disorder; tumour.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     polynucleotide sequences given in AAA26346 to AAA26458 encode the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New isolated human genes and the secreted polypeptides they encode,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Shi Y;
LA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           useful for diagnosis and treatment of e.g. cancers, neurological disorders, immune diseases, inflammation or blood disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Duan R, Moore PA,
A, Young PE, Brewer
sen HS, Mucenski M;
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Lafleur D, Wei Y, Ni J, Florence KA, Young
Soppet DR, Endress GA, Ebner R, Olsen HS, M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 11; Page 528; 634pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 98US-0095486.
98US-0095454.
98US-0095455.
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N-PSDB; AAA26447.
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens.
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Soppet DR,
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New isolated human genes and the secreted polypeptides they encode, useful for diagnosis and treatment of e.g. cancers, neurological disorders, immune diseases, inflammation or blood disorders

Disclosure, Page 36-37; 634pp; English.

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Komatsoulis GA, Rosen CA, Ruben SM, Duan R, Moore PA, Lafleur D, Wei Y, Ni J, Florence KA, Young PE, Brewer Soppet DR, Endress GA, Ebner R, Olsen HS, Mucenski M;

WPI; 2000-195282/17.

(HUMA-) HUMAN GENOME SCI INC.

The polynucleotide sequences given in AAA26346 to AAA26458 encode the human secreted proteins given in AAY91451 to AAX91691. The human secreted proteins given in AAY91451 to AAX91691. The human secreted proteins given in AAY91451 to AAX91691. The human secreted corrected makes activities based on the tissues and cells they are expressed in. Examples of the activities are: cytostatic; humanosuppressive; antiHIV; antiHIV; antiHIMIC; antiBacterial; antidiabetic; antiasthma; antipsoriatic; and cardiant. The polynucleotides and their corresponding secreted proteins are useful for preventing, treating or antiasthma; antipsoriatic; and each sequence by determining the amount of the proteins in a sample or by determining the presence of mutations in the proteins in a sample or by determining the presence of mutations in the proteins in a sample or by determining the presence of mutations in the proteins in a sample or by determining the diagnosis or treatment of colynucleotides, based on which tissues they are most highly expressed in, and include developing products for the diagnosis or treatment of cancer, tumours, neurodegenerative disorders, developmental abnormalities and foetal deficiencies, blood disorders, diseases of the immune system, allergies, Alzheimer's and behavioural diseases, inflammation, allergies, atthrities, infections, AlbS, spinal cord injuries,

transplant rejection, diabetes, asthma, sepsis, acne, psoriasis,

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polynucleotides. Specific uses are described for each of the polynucleotides, based on which tissues they are most highly expressed in, and include developing products for the diagnosis or treatment of cancer, tumours, neurodegenerative disorders, developmental abnormalities and feetal deficiencies, blood disorders, disease of the immune system, autoimmune diseases, hepatic and renal disease, inflammation, allergies, Alzheimer's and behavioural disorders, schizophrenia, osteoporosis, arthritis, infections, AIDS, spinal cord injuries, transplant rejection, diabetes, asthma, sepsis, acne, psoriasis, cardiovascular disorders, reproductive disorders, gastrointestinal disorders, respiratory disorders and metabolic disorders. The proteins or polynomial or preservatives. The proteins are also useful for identifying their binding partners.

AAA26337 to AAA26345 and AAY91450 are sequences used in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; BAFF receptor; BAFF-R; cytostatic; hypotensive; inflammation; TNF; Tumoux Necrosis Factor; autoimmune disease; immunosuppressive; cancer; myasthenia gravis; hypertension; organ transplantation; drug screening; HIV; human immunodeficiency virus; genetic disorder; cardiovascular; renal; rheumatoid arthritis; systemic lupus erythematosus; amyloidosis; haemolytic anaemia; Chagas' disease; Garave's disease; glomerulonephritis; multiple myeloma; chromosomal mapping; tissue typing; drug screening;
 proteins in a sample or by determining the presence of mutations in the
                                                                                                                                                                                                                                                                                                                                                                                                 1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                          MARGSLRRILIKLIVIGINIALIRSVAGEQAPGTAPCSRGSSWSADLDKCMDCSTSC 56
                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MARGSLRRILRLLVLGLWLALLRSVAGEQAPGTAPCSRGSSWSADLDKCMDCA-SC 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New human BAFF receptor proteins and nucleic acids, useful for
                                                                                                                                                                                                                                                                                                                                                           21; Length 156;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    note= "Wild type Val substituted with Asn"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "Wild type Pro substituted with Gln"
                                                                                                                                                                                                                                                                                                                                         Score 274.5; DB 41;
Pred. No. 6.2e-21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human BAFF receptor (BAFF-R) mutant, V20N/P21Q.
                                                                                                                                                                                                                                                                                                                                                                                               1; Mismatches
                                                                                                                                                                                                                                                                                exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAE22269 standard; Protein; 185 AA
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21-SEP-2000; 2000US-234140P.
13-FEB-2001; 2001US-268499P.
                                                                                                                                                                                                                                                                                                                                                                             96.48;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Thompson JS;
                                                                                                                                                                                                                                                                                                                                                                                               54; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2002-362428/39.
                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
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                                                                                                                                                                                                                                                                                                                      156 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         mutant; mutein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
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                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                             Matches
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The invention relates to human BAFF receptor (BAFF-R) nucleic acids and proteins. BAFF-R is a B-cell activating factor belonging to the Tumour Decrosis Factor (INF) family, which is associated with the expression of B-cells and immunoglobulins. The BAFF-R proteins, DNA and antibodies are useful for treating, preventing or delaying autoimmune diseases, cancer, tumourigenic conditions or inherited genetic disorders involving B-cells, hypertension, cardiovascular disorders, immunosuppressive diseases, renal diseases, which can be treated or prevented by BAFF-R, include systemic lupus erythematosus, rheumatoid arthritis, myasthemia gravis, autoimmune haemlytic anaemia, idiopathic thrombocycopaemia purpura, Chagas' disease Grave's disease, anti-phospholipid syndrome, Negener's granulomatosis, poly-arteritis nodosa and rapidly progressive glomeralometoris, plasma cells disorders e.g., multiple myeloma, Maldenstrom's, macroglobulinaemia, heavy-chain disease, primary or immunocyte-associated amyloidosis, and monoclomal gammopathy of undetermined significance. The nucleic acids, protein, protein homologues, and antibodies may further be used in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       percenting assays, in detection assays (chromosonal mapping, tissue typing or forensic biology), predictive medicine (e.g. diagnostic or prognostic assays, monitoring clinical trials, or pharmacogenomic). The polypeptides are further useful as immunogens to raise anti-BFFR antibodies, or in screening drugs or compounds that modulate BAFF-R activity or expression. The present sequence is human BAFF-R protein mutant.

Note: The present sequence is not shown in the specification but is derived from human BAFF-R referred as SEQ ID NO: 5 (AAE22242) and shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         --E 107
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         62 ESVGAGAGEAALPLPGLLFGAPALLGLALVLALVLVGLVSWRRRORRLRGASSAEAPDGD 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6 RSLRGRDAPAPTPCNQAECFDLLVRHCVACGLLRTPRPRPK----AGAASSPAPRTALQPQ 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23 RSVAGEQAPGTAPCSRGSSWSADLDKCMDCASCRA-RPHSDFCLGCAAAPPAPFRLLWP-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     39;
treating, preventing or delaying e.g. autoimmune diseases, cainherited genetic disorders involving B-cells, cardiovascular disorders, or renal disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 185;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human BAFF receptor (BAFF-R) mutant, V20N/P21Q/A22T/L27P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            --ILGGA---LSLTFVLGL-LSGFLVWRRCRR-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15.5%; Score 94.5; DB 23; 27.8%; Pred. No. 0.053; tive 13; Mismatches 39;
                                                                                                          Example 17; Page -; 164pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAE22266 standard; Protein; 185 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              fig 2d of the specification.
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Matches 35; Conserv
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The invention relates to human BAFF receptor (BAFF-R) nucleic acids and proteins. BAFF-R is a B-cell activating factor belonging to the Tumour Necrosis Pactor (TNF) family, which is associated with the expression of B-cells and immunoglobulins. The BAFF-R proteins, DNA and antibodies are useful for treating, preventing or delaying autoimmune diseases, cancer, tumourigenic conditions or inherited genetic disorders involving B-cells, hypertension, cardiovascular disorders, immunosuppressive diseases, renal disorders, inflammation, organ transplantation and HIV. Autoimmune diseases, which can be treated or prevented by BAFF-R, include systemic lupus erythematosus, rheumatoid arthritis, myasthenia gravis, autoimmune haemolytic anaemia, idiopathic thrombocytopaenia purpura, Chagas disease, anti-phospholipid syndrome, Wegener's granulomatosis, poly-arteritis nodosa and rapidly progressive glomerulonephritis. Plasma cells disorders e.g., multiple myelona, Waldenstrom's macroglobulinaemia, monoclonal gammopathy of undetermined significance. The nucleic acids, protein, protein homologues, and antibodies may further be used in screening assays, in detection assays (chromosomal mapping, tissue typing or forensic biology), predictive medicine (e.g. diagnostic assays, monitoring clinical trials, or pharmacogenomic). The polypeptides are further useful as immunogen to raise anti-BFR antibodies, or in screening drugs or compounds that modulate BAFF-R activity or expression. present sequence is human BAFF-R protein mutant. e: The present sequence is not shown in the specification but is ived from human BAFF-R referred as SEQ ID NO: 5 (AAE22242) and shown New human BAFF receptor proteins and nucleic acids, useful for treating, preventing or delaying e.g. autoimmune diseases, cancers, inherited genetic disorders involving B-cells, cardiovascular substituted with Asn" /note= "Wild type Leu substituted with Pro" 'note= "Wild type Pro substituted with Gln" 'note= "Wild type Ala substituted with Thr" 'note= "Wild type Val Location/Qualifiers Example 17; Page -; 164pp; English. fig 2d of the specification. or renal disorders 18-SEP-2000; 2000US-233152P. 21-SEP-2000; 2000US-234140P. 13-FEB-2001; 2001US-268499P. 14-AUG-2001; 2001US-312185P. 06-SEP-2001; 2001WO-US28006. Thompson JS; WPI; 2002-362428/39. (BIOJ) BIOGEN INC. Misc-difference 27 185 AA; Misc-difference Misc-difference Misc-difference WO200224909-A2 Ambrose CM, 28-MAR-2002 disorders, Sequence derived

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6 RSLRGRDAPAPTPCNOTECFDPLVRHCVACGLLRTPRPKP----AGAASSPAPRTALOPO 61
                                                           23 RSVAGEQAPGTAPCSRGSSWSADLDKCMDCASCRA-RPHSDFCLGCAAAPPAPFRLLWP-
                              39;
DB 23; Length 185;
                              Indels
   0.086;
                                Mismatches
15.2%; Score 92.5; 27.8%; Pred. No. 0.
                              13;
                             35; Conservative
            Local Similarity
Query Match
                           Matches
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---E 107

--ILGGA---LSLTFVLGL-LSGFLVWRRCRR----

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62 ESVGAGAGEAALPLPGLLFGAPALLGLALVLALVLVGLVSWRRRQRRLRGASSSEAPDGD 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; BAFF receptor; BAFF-R; cytostatic; hypotensive; inflammation; TNF; Tumour Necrosis Factor; autoimmune disease; immunosuppressive; cancer; myaschenia gravis; hypertension; organ transplantation; drug screening; HIV; human immunodeficiency virus; genetic disorder; cardiovascular; renal; rheumatoid arthritis; systemic lupus erythematosus; amyloidosis; haemolytic anaemia; Chagas' disease; Grave's disease; glomerulonephritis; multiple myeloma; chromosomal mapping; tissue typing; drug screening;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human BAFF receptor (BAFF-R) mutant, V20N/P21Q/A22T.
                                                                                                                                                                                                                                                                                                                                                                       AAE22267 standard; Protein; 185 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                      108 RSSPPP 113
                                                                                                                                   : : | |
122 KDAPEP 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            mutant; mutein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25-JUL-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAE22267;
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'note= "Wild type Val substituted with Asn" 'note= "Wild type Pro substituted with Gln" /note= "Wild type Ala substituted with Thr" Location/Qualifiers Misc-difference 20 Misc-difference Misc-difference WO200224909-A2

28-MAR-2002

06-SEP-2001; 2001WO-US28006 18-SEP-2000; 2000US-233152P

21-SEP-2000; 2000US-234140P. 13-FEB-2001; 2001US-268499P. 14-AUG-2001; 2001US-312185P.

(BIOJ) BIOGEN INC.

Thompson JS; Ambrose CM,

WPI; 2002-362428/39.

New human BAFF receptor proteins and nucleic acids, useful for treating, preventing or delaying e.g. autoimmune diseases, cancers, inherited genetic disorders involving B-cells, cardiovascular disorders, or renal disorders

Example 17; Page -; 164pp; English.

proteins. BAFF-R is a B-cell activating factor belonging to the Tumour Necrosis Factor (TNF) family, which is associated with the expression of B-cells and immunoglobulins. The BAFF-R proteins, DNA and antibodies are useful for treating, preventing or delaying autoimmune diseases, cancer, tumourigenic conditions or inherited genetic disorders involving B-cells, hyperension, cardiovascular disorders, immunosuppressive diseases, renal diseases, which can be treated or prevented by BAFF-R, include systemic diseases, which can be treated or prevented by BAFF-R, include systemic lupus erythemacosus, rheumatoid arthritis, myasthenia gravis, autoimmune haemolytic anaemia, idiopathic thrombocytopaenia purpura, Chagas' disease Grave's disease, anti-phospholipid syndrome, Wegener's granulomatosis, poly-arteritis nodosa and rapidly progressive glomerulomephritis. Plasma The invention relates to human BAFF receptor (BAFF-R) nucleic acids and

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cells disorders e.g., multiple myeloma, Waldenstrom's, macroglobulinaemia, heavy-chain disease, primary or immunocyte-associated amyloidosis, and monoclonal gammopathy of undetermined significance. The nucleic acids, protein, protein homologues, and antibodies may further be used in screening assays, in detection assays (chromosomal mapping, tissue typing or forensic biology), predictive medicine (e.g. diagnostic or prognostic assays, monitoring clinical trials, or pharmacogenomic). The proprestic are further useful as immunogens to raise anti-BFFR antibodies, or in Screening drugs or compounds that modulate BAFF-R activity or expression. The present sequence is human BAFF-R protein mutant.

Note: The present sequence is not shown in the specification but is derived from human BAFF-R referred as SEQ ID NO: 5 (AAE22242) and shown in fig 2d of the specification.
          8888888888888888888888888
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185 AA; Sequence

23 RSVAGEQAPGTAPCSRGSSWSADLDKCMDCASCRA-RPHSDFCLGCAAAPPAAPRLLWP- 80 6 RSLRGRDAPAPTPCNQTECFDLLVRHCVACGLLRTPRPKP----AGAASSPAPRTALQPQ 61 Query Match
15.2%; Score 92.5; DB 23; Length 185;
Best Local Similarity 27.8%; Pred. No. 0.086;
Matches 35; Conservative 13; Mismatches 39; Indels 39; Gaps à g ò

----ILGGA---LSLTFVLGL-LSGFLVWRRCRR------E 107 81 ---

108 RSSPPP 113

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: : | | 122 KDAPEP 127

Search completed: February 11, 2004, 10:38:06 Job time: 41 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

Run on:

February 11, 2004, 10:36:33 ; Search time 21 Seconds (without alignments) 522.059 Million cell updates/sec

US-10-062-599-59 608 Title: Perfect score: Sequence:

1 MARGSLRRLLRLLVLGLWLA.....LSGFLVWRRCRRERSSPPPX 114

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283308 seqs, 96168682 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR 76:*
1: Dir1:*
2: Dir2:*
3: Dir3:*
4: Dir4:* 4 3 2 1

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	probable chitinase	probable export pr	flagellar biosynth	hypothetical prote	hypothetical prote	hypothetical prote	hypothetical prote	2	ribonuclease (EC 3	conserved hypothet	fibrillin-1 precur	probable transcrip	probable amino aci	glypican precursor	probable beta-lact	hypothetical prote	Fas antigen precur	conserved hypothet	osmoregulated prol	hypothetical prote	probable protein k	diheme cytochrome	glycoprotein precu	receptor-type prot	bone marrow stroma	oligopeptide trans	receptor-like tyro	receptor tyrosine	receptor-like tyro
SUMMARIES	ID	T04484	878698	AD0753	B70939	T20910	B87353	T22758	660695	T04420	D75303	A55624	T36798	E95850	I56545	D75330	C70893	JC2395	B69092	E75138	B61213	T00872	T46966	GNVUUK	I50615	JC4390	AH3572	160	S47489	S51604
	DB	5	7	7	7	7	7	7	~	7									⊣			7		Н					7	7
	Length		245	245	436	635	519	768	261	227	346	2871	175	467	558	424	587	324	431	484	480	683	384	1008	1013	319	332	893	868	981
æ	Query	12.9	12.6	12.6	12.4	12.4	12.3	12.2	12.1	12.0	11.9	11.8	11.7	11.6	11.5	11.4	11.4	11.3	11.3	11.3	11.2	11.2	11.1	11.1	11.1	11.0	11.0	11.0	11.0	11.0
	Score	78.5	76.5	76.5	75.5	75.5	74.5	74	73.5	73	72.5	72	71	70.5	70	69.5	69.5	69	68.5	68.5	99	68	•	67.5	67.5	67	67	29	67	29
	Result No.	1	7	е	4	Ŋ	9	7	80	σ	10	11	12	13	14	72	16	17	18	19	20	21	22	23	24	25	26	27	28	29

receptor tyrosine	probable MFS trans	hypothetical prote	conserved hypothet	structural polypro	reverse transcript	trophozoite cystei	notch 3 protein -	hypothetical prote	probable export pr	flagellar biosynth	flagellar biosynth	hypothetical prote	serine/threonine-s	notch3 protein - h	conserved hypothet
849015	C82987	C36942	E83085	GNWVR3	T07965	A42125	S45306	T49381	B36869	G90964	G85812	F83545	T02731	S78549	F82989
N	7	N	~	н	N	7	~	7	N	~	~	N	~	~	~
1005	389	394	549	992	1053	1766	2318	214	245	245	245	206	884	2321	196
0	6.0	10.9	10.9	10.9	10.9	10.9	10.9	10.8	10.8	10.8	10.8	10.8	10.8	10.8	10.7
11.	Н						10	S	Ŋ	ß	L)	2	LΩ		
67 11.	66.5	99	99	99	99	99	ĕ	65.5	92	. 69	65	65.5	65.	65.5	65

ALIGNMENTS

RESULT 2

Probable export protein flip precursor - Salmonella typhimurium C;Species: Salmonella typhimurium C;Becies: Ol-Reb-1999 #sequence_revision Ol-Reb-1999 #text_change 21-Jul-2000 C;Accession: S78698 R;Ohnishi, K; Fan, F; Schoenhals, G.J.; Kihara, M.; Macnab, R.M.
J. Bacteriol. 179, 6092-6099, 1997 A;Accession: S78696; MuID:97464436; PMID:9324257 A;Accession: S78696; MuID:97464436; PMID:9324257 A;Accession: S78696 MiD:97464436; PMID:9324257 A;Accession: S78696; MuiD:97464436; PMID:9324257 A;Moscule type: DNA A;Moscule type: DNA

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A Status: preliminary; nucleic acid sequence not shown, translation not shown A, Status: b.NA A, Molecule type: DNA A, Molecule type: DNA A; Residues: 1-416 <CCL>A; Cross-references: GB:AL021929; GB:AL123456; NID:g3242291; PIDN:CAA17338.1; PID:e12524: A; Experimental source: strain H37Rv A; Experimental source: strain H37Rv A; GGenetics: A, Genetics: A, 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A, Experimental source: clone F14F7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
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                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 35; Conserv
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A; Residues: 1-635 <WI2>
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A;Description: may be involved in flagellar assembly; may be involved in export of flage C;Superfamily: flagellar biosynthetic protein flip C;Keywords: flagellum; transmembrane protein F;1-21/Domain: signal sequence #status predicted <SIG>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        flagellar biosynthetic protein FliP [imported] - Salmonella enterica subap, enterica sed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Species: Salmonella enterica subsp. enterica serovar Typhi
A;Note: this species has also been called Salmonella typhi
C;Daccession: AD0753
R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, K.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; A;Accession: AD0753
A;Reference number: AB0502; WUID:21534947; PMID:11677608
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C;Species: Mycobacterium tuberculosis
C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999
C;Accession: B70939
B;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Daviese, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S. Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998
A;Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Althors: Deciphering the biology of Mycobacterium tuberculosis from the complete genome A;Reference number: A70500; MUID:98295987; PMID:9634230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6 LRRLLRLLRLLKUGLWLALLRSVAGEQAPG--TAP-CSRGSSWSADLDKCMDCASCRARP--- 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6 LRRILIRLILVLGIMLALLRSVAGEQAPG--TAP-CSRGSSWSADLDKCMDCASCRARP--- 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                     F;22-245/Product: probable export protein filip #status predicted <MAT>
F;45-61/Domain: transmembrane #status predicted <TMI>
F;89-105/Domain: transmembrane #status predicted <TM2>
F;89-205/Domain: transmembrane #status predicted <TM3>
F;212-228/Domain: transmembrane #status predicted <TM3>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      27;
                                                                                                                                                                                                                                                                                                                                                                                                                                          12.6%; Score 76.5; DB 2; Length 245; 30.8%; Pred. No. 4.3; tive 9; Mismatches 38; Indels 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12.6%; Score 76.5; DB 2; Length 245; 30.9%; Pred. No. 4.3; tive 9; Mismatches 38; Indels 2'
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  60 --HSDF------
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33; Conservative
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A;Molecule type: DNA
A;Residues: 1-245 <PAR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ---HSDF--- 09
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Best Local S
Matches 33
                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local
Matches 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     B70939
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A;Reference number: Z19345
A;Accession: T20910
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-635 cMIL>
A;Cross-references: EMBL;Z81503; PIDN:CAB04115.1; GSPDB:GN00021; CESP:ZK1010.9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: EMBL:Z82083; PIDN:CAB04975.1; GSPDB:GN00021; CESP:ZK1010.9 A;Experimental source: clone ZK1010
                                                                                                                                                                                                                                                                                                                92 PITAYKNGGLSF---LIAYVVCGILFAVPAIHMEFALGQYAAKSPPAAFRRMMPILEGVG 148
                                                                                                                                                                                                 142 MPSGTARARIILITEVGVGAALTAVVAATLSFVPDQHPLSRNIHLLMTAAVAMAISAAICR 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        31 PGTAPCSRGSSWSADLDKCMDCASCRARP--HSDFCLG--CAAAPPAPFRLLWPILGGAL 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    hypothetical protein ZK1010.9 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 21-Jan-2000
C;Accession: T20910; T27646
                                                                                                                                      1 MARGSLRRILLRLLVLGLWLALLRSVAGEQA--PGTAPCSRGSS--WSADLDKCMDCASCR
                                                                        Gaps
                                                                     49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7;
12.4%; Score 75.5; DB 2; Length 436; larity 23.0%; Pred. No. 8.4; Conservative 16; Mismatches 52; Indels 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 2; Length 635;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              B87353
hypothetical protein CC0837 [imported] - Caulobacter crescentus
C;Species: Caulobacter crescentus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Map position: 3
A;Introns: 71/3; 184/2; 316/3; 403/1; 444/3; 547/3; 577/3
C;Superfamily: gamma-aminobutyric acid transporter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28;
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                                                                                                                                                                                                                                                                                                                                                                                                       ------ALSLIFVLGLLSGFLVWRRCR 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 260 AVPGDQPDEVVÁVVÍFVCVGLÍGGIALMNŘVŘ 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   submitted to the EMBL Data Library, November 1996 A;Reference number: Z20398 A;Accession: T27646
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12.4%; Score 75.5; Di
36.6%; Pred. No. 11;
tive 10; Mismatches
                                                                                                                                                                                                                                                                       57 ARPHSDFCLGCAAAPPAPFRLLW-
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A;Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: funct A;Reference number: A69000; MUID:98037514; PMID:9371463
A;Accession: 669099
A;Accession: 669099
A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Residue: Lype: DNA
A;Residues: 1-261 < ANTHA
A;Residues: 1-261 < ANTHA
A;Crosser-references: GB:AE000929; GB:AE000666; NID:g2622853; PIDN:AAB86210.1; PID:g262287
A;Experimental source: strain Delta H
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C; Accession: D75303
R; White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.; I, M.; Shen, M.; Yahan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Mals.; Snuth, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
A; Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
A; Reference number: A75250; MUID: 20036896; PMID: 10567266
A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4
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A,Residues: 1-227 <RGS>
A,Cross-references: EMBL.AF000940; NID:g2150001; PIDN:AAB58719.1; PID:g2150002
A,Experimental source: cv. Igri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    191 PGSTVKNKTGSWRTFKPVLDKDKCIDCDNCILFCPEGCINREHEIDYDYCKGCGICAEKC 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 91 LLSSLRAEWPTLACPASDGLQFWAHEWEKHGTCAQNLFHEHGYF---QTAAPPRPAPLLD 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                --RPHS---DFCLGCA-AAPPA 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21 LLRSVAGEQAPGTAPCSRG-SSWSADLDKCMDCASCRARPHSDFCLGCAAAPPAPFRLLW 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ribonuclease (EC 3.1.-.-) - barley
C;Species: Hordeum vulgare (barley)
C;Daccies: Hordeum vulgare (barley)
C;Daccession: 10420
C;Accession: To Rogers, S.W.
S;Rogers, J.C.; Rogers, S.W.
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C;Species: Deinococcus radiodurans
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 17-Mar-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17;
                                                                                                                                                                                                                                                                                                                                                                                                                       Length 261;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ch 12.0%; Score 73; DB 2; Length 227; Il Similarity 30.0%; Pred. No. 8.8; 30; Conservative 11; Mismatches 45; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               80 PIL-----GGALSLIFVLGLL---SGFLVWRRCRRERS 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21;
                                                                                                                                                                                                                                                                                                                                                                                                                       DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             31 PGTAPCSRGSSWSA----DLDKCMDCASCRA-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A,Accession: T04420
A,Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 12.1%; Score 73.5; Di
Best Local Similarity 29.2%; Pred. No. 8.8;
Matches 19; Conservative 8; Mismatches
                                                                                                                                                                                                                                                                                                                     C;Superfamily: pyruvate synthase gamma chain C;Keywords: coenzyme A; oxidoreductase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C'Genetics:
87/3; 87/3
C'Superfamily: Enterobacter ribonuclease
C'Keywords: hydrolase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Reference number: Z15355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                251 PVKAI 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     74 PFRLL 78
                                                                                                                                                                                                                                                                                        A; Gene: MTH1740
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                          C,Accession: B87353 Forger C. P. Paulsen, I.T.; Nelson, K.E.; Bisen, J.; Heidelberg, J. B.; Laub, M.T.; DeBoy, M.T.; Dodson, K.T.; Dodson, K.T.; Oukin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon D. J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M. A; Title: Complete Genome Sequence of Caulobacter crescentus.

A,Reference number: A87249; MUID:21173698; PMID:11259647

A,Statutus: preliminary

A,Rodecule type: DNA

A,Residues: 1-519 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              probable pyruvate synthase (EC 1.2.7.1) gamma chain - Methanobacterium thermoautotrophid (5,Species: Methanobacterium thermoautotrophicum (5,Species: Methanobacterium thermoautotrophicum (5,Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 05-May-2000 (5,Accession: G69099 R.Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.; Qiu, D. S.; Shutch, G.W.; Vicainie, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiwani, N. Ki, S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N. J. Bacteriol. 179, 7135-7155, 1997
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                                                                                                                                                                                                                                                                                                                                            A; Cross-references: GB: AE005673; NID: 913422090; PIDN: AAK22822.1; GSPDB: GN00148
C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 310 IVSRDAALLSQVLLRVLYMVPIAFVMVRGAESLPPAWALAGGPAAAVTFLAGQVAGSLIMIT 369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ASEAUS: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-768 <MIL>
A;Cross-references: EMBL:281091; PIDN:CAB03142.1; GSPDB:GN00019; CESP:F55H12.1
A;Experimental source: clone F55H12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     52 CASCRARPHSDFCLGCAAAPPAPFRLL------WPILGGALSLTFVLGLLSGFLVWRR 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 17-Mar-2000
Accession: T22758
   C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 20-Apr-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        --SWSADLDKCMD
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A;Introns: 114/3; 189/1; 301/2; 426/3; 513/1; 554/3; 657/3; 687/3; 741/1
C;Superfamily: gamma-aminobutyric acid transporter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        153 CAFVFAVPAIHMEFALGQYAAKSPPAVFRRIMPALEGVGWMTCIVGAVIG 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 2; Length 519;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 768
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Pred. No. 18;
7; Mismatches 19; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       hypothetical protein F55H12.1 - Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R;Dobson, R. submitted to the EMBL Data Library, October 1996 A;Reference number: 219610 A;Recession: T22758
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12.3%; Score 74.5; D
24.3%; Pred. No. 12;
:ive 21; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9 LLRLLVLGLWLALLRS-VAGEQAPGTAPCSRGS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                104 CRRERS-----SPPP 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              370 VSAEDTPDLLAISPTP 385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Species: Caenorhabditis elegans
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Best Local Similarity 40.0%;
Matches 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    33; Conservative
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Best Local Similarity
Matches 33; Conservat
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                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Gene: CC0837
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g à g ò

52;

10; Mismatches

2;

DB

Score 72.5; | Pred. No. 13;

11.9%; 28.8%;

Query Match 11.9 Best Local Similarity 28.8 Matches 32; Conservative

업 à

A; Map position: 1

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A; Residues: 1-467 «KIR»
A; Cross-references: GB: ALS91985; PIDN: CAC48469.1; PID: G15139941; GSPDB: GN00167
A; Cross-references: Strain 1021, megaplasmid psymb
A; Experimental source: strain 1021, megaplasmid psymb
B; Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler, pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.;
L.; Hyman, R.W.; Jones, T.
Science 293, 668-672, 2001
A; Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, B.; Komp, C.; Lelaure, hebault, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K. A; Reference number: A96039; MUID: 21368234; PMID: 11474104
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A;Residues: 1-558 RRES>
A;Cross-references: GB:L14067; NID:g506416; PIDN:AAA41251.1; PID:g506417
A;Cross-references: GB:L14067; NID:g506416; R.K.; Margolis, R.V.; Margolis, R.U.
B;Crem. Biophys. Res. Commun. 188, 395-401, 1992
A;Title: Cloning of a major heparan sulfate proteoglycan from brain and identification a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      probable amino acid carrier protein [imported] - Sinorhizobium meliloti (strain 1021) me Cispecies: Sinorhizobium meliloti
Cispecies: Sinorhizobium meliloti
Cidate: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 30-Sep-2001
CiAccession: B59850
Rifinan, T.M.; Weidner, S.; Wong, K.; Buhrmester, J.; Chain, P.; Vorholter, F.J.; Hernar. Proc. Natl. Acad Sci. US.S. 98, 9889-9894, 2001
A;Title: The complete sequence of the 1.683-4b pSymB megaplasmid from the N2-fixing endc. A;Reference number: A95842; MUID:21396508; PMID:11481431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ........ weuronal expression of glypican, a cell-surface glycosylphosphatidylinositol-an A;Reference number: I56545; MUID:94267529; PMID:8207484
                                                                                                                              5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7
                                                                                                                                                                                                                       || :|||; : :|| :| | :| | 49 ARDALRRVAFVRAAQRVGIPLATIREALAELPEGRIPTEDDWARLSESWRSELDERIKQL 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    | ::| |:| |: | : | : | 322 LAIMVSGVWASGETGAVLSSAAFEAALDG----YGNYLVTISLALFAFTTILGWAYYAE 376
                                                                                                                                                                                        23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  --- SWSADLD 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      glypican precursor - rat
Cispecies: Rattus norregicus (Norway rat)
Cibate: 26-Jul-1996 #sequence revision 26-Jul-1996 #text_change 31-Jan-2000
CiAccession: I56545; JC1281; PC1132
Rilitwack, B.D.; Stipp, C.S.; Kumbasar, A.; Lander, A.D.
A. Neurosci. 14, 3713-3724, 1994
A;Title: Neuronal expression of glypican, a cell-surface glycosylphosphatidy
                                                                                                                                                                                  --CSRGSSWSADLDKCMDCA
                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                              26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Gene: SMD20069
A;Genome: plasmid
C;Superfamily: sodium-dependent D-alanine/glycine transport protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 467;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
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                                                                                                                                                                                                                                                                                                                                                               ---GCLSLETCVL 131
                                                                                                                                                                                                                                                                                                    92
                                                                                                                                                                                                                                                                                                 54 SCRARPHSDFCLGCAAAPPAPFRLLWPILGGALSL-TFVL
                                                                                                                        33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21;
                                                                                                                                                                                  2 ARGSLRRLLRLLV---LGLWLALLRSVAGEQAPGTAP---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10 LRLLVLGLWL----ALLRSVAGEQA-PGTAPCSRGS--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                               ed. No. 11;
Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11.6%; Score 70.5; I
26.4%; Pred. No. 26;
                                                                                               Pred. No.
                                                                                29.0%; Pred
                                                                                                                        29; Conservative
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                                                                                                                                                                                                                                                                                                                                                           109 N-RLRDHLTDCIGC-
                                                                                            Best Local Similarity
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Matches 28; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Status: preliminary A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Accession: E95850
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                                                                                                                        Matches
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A; Molecule type: DNA
A; Residues: 1-346 <WHI>
A; Cross-references: GB: AE002053; GB: AE000513; NID: g6459999; PIDN: AAF11754.1; PID: g646000
A; Experimental source: strain R1
C; Genetics:
A; Gene: DR2205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C; Accession: A55624

% Yili, W. Smiley, E.; Germiller, J.; Sanguineti, C.; Lawton, T.; Pereira, L.; Ramirez, J. Biol. Chem. 270, 1798-1806, 1995

A; Fitle: Primary structure and developmental expression of Fbn-1, the mouse fibrillin ge

A; Reference number: A55624; MUID:95130561; PMID:7829516
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               T36798

probable transcription regulator soxR-like - Streptomyces coelicolor
C;Species: Streptomyces coelicolor
C;Species: O3-Dec-1999 #sequence_revision O3-Dec-1999 #text_change O7-Dec-1999
C;Accession: T36798
R;Oliver, K.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A. submitted to the EMBL Data Library, July 1999
A;Reference number: Z21614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Cross-references: EMBL: AL096811; PIDN: CAB46795.1; GSPDB: GN00070; SCOEDB: SCI30A.18c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   87 LLIVICVGLGVL--TÄGSASPWTV-----MWVGALVAAFGAVLATVWHLRPAGSLFFVFA 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                  64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Date: 23-Mar-1995 #sequence_revision 23-Mar-1995 #text_change 02-Aug-2002; Accession: A55624
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12 LLVLGLWLALLRSVAGEQAPGTAPCSRGSSWSADLDKCMDCASC---RARPHSD----FC
                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;Status: preliminary
;Molecule type: mRNA
;Residues: 1-2871 <YIN>
;Cross-references: GB:L29454; NID:g575509; PIDN:AAA56840.1; PID:g575510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              65 LGCAAA--PPAPFRLLWPILGGALSLTFVLGLLSGFLVWRRCRRERSSPPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 2; Length 2871; 75;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 2; Length 175;
                                                                                                                                                                                                                                                                                                                                                                                       Indels
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24; -CASCRARPHS

7; Mismatches

36 CSRGSSWSADLDKCMD-

ద à g

2100 PTEPDEAFRQICPFGSGII 2118

68 AAAPPAPFRLLWPILGGAL 86

Score 72; Pred. No.

11.8%; 25.3%;

Conservative

Local Similarity nes 20; Conserv

Query Match Best Local S: Matches 20

C, Superfamily: fibrillin 1; EGF homology R;1201-1236/Domain: EGF homology <EGF>

Genetics:

fibrillin-1 precursor - mouse C;Species: Mus musculus (house mouse)

Accession: A55624

A; Status: preliminary; translated from GB/EMBL/DDBJ

A; Molecule type: DNA A; Residues: 1-175 <OLI>

11.7%; Score 71;

A; Experimental source: strain A3(2) C; Genetics: A; Gene: SCOEDB: SCI30A, 18c

Genetics: Gene: SCOEDB:SCI30A,18c

Query Match

A; Reference number: JC1281; MUID: 93038690; PMID: 1417860

```
A.Molecule type: protein
A.Residues: 24-55,424-445 < KA2>
A.Residues: 24-56,424-445 < KA2>
B.Superfamily: glypican
B.Status predicted < SIG>
F.1-23/Domain: signal sequence #status predicted < MAT>
F.24-530/Product: glypican #status predicted < MAT>
F.55-466,488,490/Binding site: heparan sulfate (Ser) (covalent) #status predicted
F.79,116/Binding site: carbohydrate (Asn) (covalent) #status predicted
F.799,512/Binding site: carbohydrate (Thr) (covalent) #status predicted
F.530/Modified site: GPI-anchor ethanolamine amidated carboxyl end (Ser) (in mature form
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R.J.;
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A;Molecule type: DNA
A;Residues: 1-424 <WHI>
A;Cross-references: GB:AE002036; GB:AE000513; NID:g6459766; PIDN:AAF11537.1; PID:g645977
A;Experimental source: strain R1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1. A;Reference number: A75250; MUID:20036896; PMID:10567266 A;Accession: D75330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Accession: D75330
K;White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11 RLLVLGLWLA--LLRSVAGEQAPGTAPCSRGSSWSADLDKCMDCASCR----ARPHSDFC 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3 RGSLRRLLRLLVLGLWLALLRSVAGEQAPGTAPCSRGSSWSADLDKCMDCASCRA---- 57
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C.Species: Deinococcus radiodurans
C.Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 31-Mar-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
A;Molecule type: mrNa
A;Residues: 1-20, T', 22-311, Y',313-361, A',363-514, I',516-558 <KAR>
A;Cross-references: GB:L02896; NID:g204424; PIDN:AAA86439.1; PID:g204425
A;Experimental source: brain
A;Accession: PC1132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 70; DB 2; Length 558;
Pred. No. 33;
6; Mismatches 19; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    35; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             probable beta-lactamase - Deinococcus radiodurans (strain R1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           58 ----RPHSDFCLGCAAA-----PPAPFRLLWPILGGALSL 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   59 PAVSAPAADGCLPAAPAVTQAPRPPQP-----LSGRLGL 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 37.7%;
Matches 26; Conservative
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Best Local Similarity
Matches 30; Conserv
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us-10-062-599-59.rsp

GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on:

February 11, 2004, 10:32:48; Search time 13 Seconds (without alignments) 412.389 Million cell updates/sec

Title: Perfect score:

US-10-062-599-59 608 1 MARGSLRRLLRLUVLGLWLA......LSGFLVWRRCRRERSSPPPX 114 Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

127863 segs, 47026705 residues Searched:

127863 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_41:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Q9np84 homo sapien	m tum		œ	Q9wvh9 mus musculu	P54700 salmonella	-	O15118 homo sapien	Q61554 mus musculu	Q9wvj9 mus musculu	ratt	Q24400 drosophila		homo	rattu	O15499 homo sapien		Q9bzj7 homo sapien		P54755 gallus gall		Q62424 mus musculu	P54757 rattus norv	Q9tv36 sus scrofa	055058 cricetulus		P08563 rubella vir	Q9y219 homo sapien	Q61982 mus musculu	Q9r172 rattus norv	P33133 escherichia	Q9um47 homo sapien	о пото
SUMMARIES	al Ba	1 FN14 HUMAN	1 FN14 MOUSE	1 T13C HUMAN				PORD	1 NPC1 HUMAN	FBN1	FBL4	GPC1	_	1 PTTG_HUMAN	Y127		1 GSCL_HUMAN	1 YG84 METTH	1 GP62_HUMAN	1 VGLM_UUK	1 EPAS_CHICK	1 BST1_RAT	1 HXAD_MOUSE	1 EPAS_RAT	FBN1	FBL4	Y6B9	POLS	JAGS	NTC3	NTC3		_	1 HRA3_HUMAN
	Length	129					245		1278					180	314	324	205	431				319			~1		394					245		453
de	Match	93.5	73.2		•	12.7	12.6	12.1	٠		11.5		11.4	11.3	11.3	11.3	11.3	11.3	11.1	11.1	11.1	11.0	11.0	17.	11.0	10.9	10.9	10.5	10.9	10.5	0	10.8	10.8	10.7
	Score	571	445	87	78		76.5	ന	72	72	70	7	69.5	69	69	69	68.5	68.5	67.5	67.5	67.5	49	67	67	lo	99				99	9	65.5	'n.	65
	Result No.	т	7	m	4	2	9	7	6 0	on	10	11	12	13	14	. 15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33

O08644 mus musculu	P23470 homo sapien	Q03499 hepatitis e	O95407 homo sapien	095967 homo sapien	Q01279 mus musculu	P16283 mus musculu	P49862 homo sapien	075880 homo sapien	P17129 canis famil	P71809 mycobacteri	P83105 homo sapien	
EPB6_MOUSE	PTPG HUMAN	VST1_HEVME	TR6B_HUMAN	FBL4 HUMAN	EGFR MOUSE	B3A3 MOUSE	KLK7 HUMAN	SCO1_HUMAN	PSPB_CANFA	PYRC MYCTU	HRA4_HUMAN	
rd	-	~1	, 	н	н	Н	٦	Н	Н	Н	Н	
1014	1445	123	300	443	1210	1227	253	301	363	430	476	
10.7	10.7	10.6	10.6	10.6	10.5	10.5	10.4	10.4	10.4	10.4	10.4	
65	65	64.5	64.5	64.5	64	64	63.5	63.5	63.5	63.5	63.5	
34	32	36	37	38	39	40	41	42	43	44	45	

ALIGNMENTS

MEDLINE=21585797; PubMed=11728344;

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                                                                                                                                                                                                                                                                                                                                                                              INDUCTION: By fibroblast growth factor 1 (FGF1) and phorbol ester. SIMILARITY: Contains 1 TNFR-Cys repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MARGSLRRLLRLLVLGLWLALLRSVAGEQAPGTAPCSRGSSWSADLDKCMDCASCRARPH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MARGSLRRLLRLLVLGLWLALLRSVAGEQAPGTAPCSRGSSWSADLDKCMDCASCRARPH
              Wiley S.R., Cassiano L., Lofton T., Davis-Smith T., Winkles J.A.,
Lindher V., Liu H., Daniel T.O., Smith C.A., Fanslow W.C.;
"A novel TNF receptor family member binds TWEAK and is implicated in
anglogenesis.";
                                                                                                                                                       proteins.
SUBUNIT: Associates with TRAF1 and TRAF2, and probably also with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Gaps
                                                                             Immunity 15:837-846(2001).
-!- FUNCTION: Receptor for TNFSF12/TWEAK. Weak inducer of apoptosis some cell types. Promotes angiogenesis and the proliferation of endothelial cells. May modulate cellular adhesion to matrix
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SDFCLGCAAAPPAPFRLLWPILGGALSLTFVLGLLSGFLVWRRCRRERSSPPP 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SDFCLGCAAAPPAPFRLLWPILGGALSLTFVLGLLSGFLVWRRCRRRRFTTP 113
                                                                                                                                                                                                                                                                                                       ISOId=Q9NP84-2; Sequence=VSP 006519;
TISSUE SPECIFICITY: Highly expressed in heart, placenta and
kidney. Intermediate expression in lung, skeletal muscle and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  POTENTIAL.
TUMOR NECROSIS FACTOR RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 129;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 93.9%; Score 571; DB 1; Length 12: Best Local Similarity 94.7%; Pred. No. 7.3e-48; Matches 107; Conservative 0; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE; PS50050; TNFR_NGFR_2; FALSE_NEG.
Receptor; Angiogenesis; Apoptosis; Transmembrane; Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BF3FDFB9C1E1C448 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Missing (in isoform 2).
                                                                                                                                                                                                      SUBCELLULAR LOCATION: Type I membrane protein. ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                          3vent=Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            006519
                                                                                                                                                                                                                                                                           IsoId=Q9NP84-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INTERPRO; IPR001368; TNFR C6.
PROSITE; PS00652; TNFR NGFR 1; FALSE NEG.
PROSITE; PS50050; TNFR NGFR 2; FALSE NEG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /FTId=VSP
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MIM; 605914; -.
GO; GO:0006928; P:cell motility; TAS.
GO; GO:0007275; P:development; TAS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL, AF191148; AAF69108.1; -.
EMBL; AB035480; BAA94792.1; -.
EMBL; AB035481; BAB17850.1; -.
EMBL; BC002718; AAH02718.1; -.
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TRANSMEM
DOMAIN
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RA Arakawa T., Hara A., Shibata K., Yoshino M., Itoh M., Ishii Y., Rawai J., Shinagawa A., Shibata K., Komo H., Adachi J., Fukuda S., Arakawa T., Hara A., Fukunishi Y., Komo H., Adachi J., Fukuda S., Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R., Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Saito R., Radota K., Matsuda H., Ashburner M., Batalov S., Casavant T., Ra Fuell P., Lewis S., Matsuo Y., Nikaido I., Fesole G., Quackenbush J., Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T., Ra Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G., Raka J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.P., Bromstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M., Raschincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H., Lyono P., Marchiomi L., Mashima J., Mazzarelli J., Mombaerts P., Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-P., Warshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=22388257; PubMed=12477932;
A Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Altschul S.F., Zeeberg B., Wagner L., Shameno C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
A stapleton M., Soares M.B., Bonaldo M.F., Carainci P., Prange C.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Rakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
"Hench and initial analysis of more than 15,000 full-length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=BALBENC; TISSUE=Fibroblast;
MEDINE=2002039; PubMed=10551889;
MEDINE=2002039; PubMed=10551889;
Meighan-Mantha R.L., Hsu D.K.W., Guo Y., Brown S.A.N., Peng S.-L.Y.,
Peifley K.A., Alberts G.F., Copeland N.G., Gilbert D.J., Jenkins N.A.,
Richards C.M., Winkles J.A.;
"The mitogen-inducible Fn14 gene encodes a type I transmembrane
protein that modulates fibroblast adhesion and migration.";
J. Biol. Chem. 274:33166-33176(1999).
                                                                                                                                                 15-FEB-2003 (Rel. 41, Last sequence update)
15-GEP-2003 (Rel. 42, Last annotation update)
Tumor necrosis factor receptor superfamily member Fn14 precursor
(Fibroblast growth factor-inducible immediate-early response protein
14) (FGF-inducible 14) (Pibroblast growth factor regulated protein
(Tweak-receptor) (TweakR).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinge; Musin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hayashizaki Y.;
"Functional annotation of a full-length mouse cDNA collection.";
Nature 409:685-690(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         human and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUE=Cerebellum, and Placenta;
MEDLINE=21085660; PubMed=11217851;
                                                                                                           (Rel. 41, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TNFRSF12A OR FN14 OR FGFRP2. Mus musculus (Mouse).
          STANDARD;
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FN14 MOUSE
09CR75; 090ZW3;
28-FEB-2003 (Re-
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                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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EMBL; AR005530; BAB24101.1; --
EMBL; AR005530; BAB24101.1; --
EMBL; BC025860; AAH25660.1; --
EMBL; BC025860; AAH25660.1; --
MCD; MCJ:1351484; Thfrestlaa.
GC; GC:0005886; C:plasma membrane; IDA.
GC; GC:0005155; P:cell adhesion; IDA.
GC; GC:000531; P:substrate-bound cell migration, cell attach. .; IDA.
INTERPRO; IPRO1368; TNFR CG.
PROSITE; PS000652; TNFR NGFR 1; FALSE NG.
PROSITE; PS00065; TNFR NGFR 2; FALSE NG.
PROSITE; PS00065; TNFR NGFR 2; FALSE NG.
PROSITE; PS00065; TNFR NGFR 2; FALSE NG.
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FUNCTION: Receptor for INFSF12/TWEAK (By similarity). Weak inducer
                      of apoptosis in some cell types. Promotes angiogenesis and the proliferation of endothelial cells. May modulate cellular adhesion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUBUNIT: Associates with TRAF1 and TRAF2, and probably also with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                       TRAF3 (By similarity).
SUBCELLULAR LOCATION: Type I membrane protein.
TISSUB SPECIFICITY: Highly expressed in fetal heart, intestine, kidney, liver, lung and skin, and in adult heart and ovary. Intermediate expression in adult kidney, lung and skin.
INDUCTION: By fibroblast growth factor I (FGF1).
SIMILARITY: Contains I TNFR-Cys repeat.
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15-SEB-2003 (Rel. 42, Last annotation update)
17-VEB-2003 (Rel. 42, Last annotation update)
18-SEB-2003 (Rel. 42, Last annotation update)
18-SEB-2003 (Rel. 42, Last annotation update)
19-SEB-2003 (BAFF receptor (BAFF receptor)
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Mammalia; Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Receptor; Angiogenesis; Apoptosis; Transmembrane; Signal.
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1665C68B4D9A9253 CRC64;
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28-FEB-2003 (Rel. 41, Last seq
15-SEP-2003 (Rel. 42, Last ann
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84; Conservative
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Q96RJ3;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for statement entities are agreement (See http://www.isb-sib.ch/announce/or send an email to license@ibosb.sib.ch)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Isoid=Q96RU3-2; Sequence=VSP_006505;
Note=No experimental confirmation available;
-!-TISSUE SPECIFICITY: Highly expressed in spleen and lymph node, and in resting B-cells. Detected at lower levels in activated B-cells, resting CD4+ T-cells, in thymus and peripheral blood leukocytes.
-!- SIMILARITY: Contains 1 TNFR-Cys repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              81 ------ILGGA---LSLTFVLGL-LSGFLVWRRCRR------E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIGNAL-ANCHOR (TYPE III MEMBRANE PROTEIN) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23 RSVAGEQAPGTAPCSRGSSWSADLDKCMDCASCRA-RPHSDFCLGCAAAPPAPFRLLWP-
                                                                                                                                        Ambrose C.; "BAFF-R, a newly identified TNF receptor that specifically interacts with BAFF-";
                                                                                                                                                                                                                                                                            Gaps
                 TISSUB-B-cell lymphoma, MEDLINB-21442025; PubMed-11509692; Thompson J.S., Bixler S.A., Qian F., Vora K., Scott M.L., Cachero T.G., Hession C., Schneider P., Sizing I.D., Millen C., Strauch K., Zafari M., Benjamin C.D., Tschopp J., Browning J.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     40;
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PROSITE; PS50050; TWPR NGFR 2; PALSE NEG.
Receptor; Immune response; Signal-anchor; Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EXTRACELLULAR (POTENTIAL)
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/FIId=VSP 006505.
F2BFB9B099A27138 CRC64;
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BY SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IsoId=Q96RJ3-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14.3%; Score 87; 27.0%; Pred. No.
SEQUENCE FROM N.A. (ISOFORMS 1 AND
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      184 AA; 18863 MW;
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                                                                                                                                                                                                              Science 293:2108-2111(2001)
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Mus musculus (Mouse)
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SEQUENCE FROM N.A.
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                                                                                                                                                 FBL5_RAT STANDARD; PRT; 448 AA.

Q9WHWH Q9R284;

16-OCT-2001 (Rel. 40, Created)

16-OCT-2011 (Rel. 40, Last sequence update)

15-SEP-2003 (Rel. 42, Last annotation update)

15-SEP-2003 (Rel. 42, Last annotation update)

Fibulin-5 precursor (FIBL-5) (Developmental arteries and neural crest EGF-like protein) (Dance) (Embryonic vascular EGF repeat-containing protein) (EVEC).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.

MEDLINE=99278197; PubMed=10347091;

MEDLINE=99278197; PubMed=10347091;

MEDLINE=99278197; PubMed=10347091;

MEVEC, a novel epidermal growth factor-like repeat-containing protein upregulated in embryonic and diseased adult vasculature.";

Circ. Res. 84:1166-1176(1999)

-!- FUNCTION: PROMOTES ADHESION OF ENDOTHELIAL CELLS THROUGH
-! FUNCTION: PROMOTES ADHESION OF INTERRINS AND THE RGD MOTIF: COLLS BE A VASCULAR LIGAND FOR INTEGRIN RECEPTORS AND MAY PLAY A ROLE IN VASCULAR DEVELOPMENT AND REMODELING.
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EGF-LIKE 2, CALCIUM-BINDING (POTENTIAL).
EGF-LIKE 3, CALCIUM-BINDING (POTENTIAL).
EGF-LIKE 4, CALCIUM-BINDING (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                  Rattus norvegicus (Rat).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.

MEDLINE=9937779; PubMed=10428823;
Makamura T., Ruiz-Lozano P., Lindner V., Yabe D., Taniwaki M.,
Purukawa Y., Kobuke K., Tashiro K., Lu Z., Andon N.L., Schaub R.,
Matsumori A., Sasayama S., Chien K.R., Honjo T.;
"DANCE, a novel secreted RGD protein expressed in developing,
atherosclerotic, and balloon-injured arteries.";
"J. Biol. Chem. 274:22476-22483(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE; PSO0010; ASX HYDROXYL; 4.
PROSITE; PSO1022; EGF_1; FALSE_NEG.
PROSITE; PSO1186; EGF_2; 4.
PROSITE; PSO1187; EGF_CA; 6.
Cell adhesion; Calcium-binding; Repeat; Signal; EGF-like domain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             !- SUBCELLULAR LOCATION: Secreted.
!- SIMILARITY: Belongs to the fibulin family.
!- SIMILARITY: Contains 6 EGF-like domains.
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InterPro; IPR00152; Asx hydroxyl.
InterPro; IPR001881; EGF Ca.
InterPro; IPR06209; EGF_like.
Pfam; PF00008; EGF; 4.
SMART; SM00179; EGF CA; 4.
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448
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1167
2206
246
                                              121 KDAPEP 126
          108 RSSPPP 113
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SIGNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6 LRRLLRLLVLGLWLALLRSVAGEQAPGTA - PCSRGSSWSADLDKCMDCASCRARPHSDF 63
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EGF-LIKE 6, CALCIUM-BINDING (POTENTIAL).

BY SIMILARITY.

BY SIMILAR
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MARAMLET T., Rulz-Lozano P., Lindner V., Yabe D., Taniwaki M.,
Rukawa T., Rulz-Lozano P., Lindner V., Yabe D., Taniwaki M.,
Purukawa Y., Kobuke K., Tashiro K., Lu Z., Andon N.L., Schaub R.,
Matsumori A., Sasayama S., Chien K.R., Honjo T.,
Matsumori A., Sasayama S., Chien K.R., Honjo T.,
Matsumori A., Sasayama S., Chien K.R., Honjo T.,
Indancia and balloon-injured arteries.";
J. Biol. Chem. 274:22476-22483(1999).
J. Biol. Chem. 274:22476-22483(1999).
J. Biol. Chem. 274:22476-22483(1999).
J. Biol. Chem. 274:22476-22483(1999).
J. FUNCTION: PROMOTES ADHESION OF ENDOTHELIAL CELLS THROUGH
INTERACTION OF INTEGRINS AND THE RGD MOTIF. COULD BE A VASCULAR
LIGAND FOR INTEGRIN RECEPTORS AND MAY FLAY A ROLE IN VASCULAR
DEVELOPMENT AND REMODELING.
J. SUBCELLULAR LOCATION: Secreted.
J. SUBCELLULARITY: Belongs to the fibulin family.
J. SIMILARITY: Contains 6 EGF-like domains.
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15-SEP-2003 (Rel. 42, Last annotation update)
Fibulin-5 precursor (FIBL-5) (Developmental arteries and neural crest
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        50; Gaps
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12.8%; Score 78; DB 1; Length 448; 24.1%; Pred. No. 2.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            24; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            E6BC68F7BF14B714 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      50160 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EGF-like protein) (Dance). FBLN5 OR DANCE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26; Conservative
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WEDLINE=97464436; PubMed=9324257;
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             SOLITIFIE WAS DEPARTED BY DEPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4 LKRILTVTILALWL------PHPGNAQQQCTNGFDLDRQSGQCLDIDECRTIPEA-- 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EGF-LIKE 1, DIVERCENT.

EGF-LIKE 2, CALCIUM-BINDING (POTENTIAL).

EGF-LIKE 3, CALCIUM-BINDING (POTENTIAL).

EGF-LIKE 4, CALCIUM-BINDING (POTENTIAL).

EGF-LIKE 5, CALCIUM-BINDING (POTENTIAL).

EGF-LIKE 6, CALCIUM-BINDING (POTENTIAL).

CELL ATTACHMENT SITE (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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Enterobacteriaceae; Salmonella.
NCBI_TaxID=602;
                                                                                                                                                                                                                                                    PROSITE; PS00010; ASX HYPROXYL; 4.
PROSITE; PS00022; BGF_1; FALSE_NEG.
PROSITE; PS01186; EGF_2; 4.
PROSITE; PS01187; EGF_CA; 6.
Cell adhesion; Calcium-binding; Repeat; Signal; EGF-like domain; Glycoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BY SIMILARITY.
N-LINKED (GLCNAC. . .) (POTENTIAL)
N-LINKED (GLCNAC. . .) (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 77; DB 1; Length 448;
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01-0CT-1996 (Rel. 34, Last sequence update)
28-FBZ-2003 (Rel. 41, Last annotation update)
Flagellar biosynthetic protein flip precursor.
FLIP OR FLAR OR STM1979
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pred. No. 2.8;
8; Mismatches
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send an email to license@isb-sib.ch)
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                                        EMBL, AF112151; AAD41767.1;
HSSP; P00736; 1APQ.
MGD; MGI:1346091; Fblns.
InterPro; IPR000152; Asx hydroxyl.
InterPro; IPR001981; EGF_Ca.
InterPro; IPR00509; EGF_Iike.
Fam; PF00008; EGF; 4.
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Matches 26; Conservative
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AC PS470;
DT 01-0CT-1996
DT 01-0CT-1996
DT 28-FEB-2003
DE FIAGALIAR SALMORD FILAR
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                                                                                                                                                                                                          MEDLINE=21534948; PubMed=11677699;
MCClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P., Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D., Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E., Waterston R., Wilson R.K., Waterston R., Wilson R.K., "Complete genome sequence of Salmonella enterica serovar Typhimurium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BMEL; AE008787; AAL20891.1; -.
BY EL; S78698; S78698.
StyGene, SG10577; filp.
InterPro; IPR005837; Filp.
InterPro; IPR005838; TypeIII_P.
Pfam; PF00813; PILP.
PRINTS; PR01302; TYPEIIMPROT.
PRODOM; PD002586; TypeIII_P; I.
PRINTS; PR01103; filp; I.
PROSITE; PS01060; FLIP_1; I.
PROSITE; PS01060; FLIP_1; I.
PROSITE; PS01061; FLIP_2; I.
PROSITE; FN01061; FLIP_2; I.
PROSITE; PS01061; FLIP_2; I.
PROSITE; PS01061; FLIP_2; I.
PROSITE; FN01061; FLIP_2; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FUNCTION: Plays a role in the flagellum-specific transport system 'PUNCTION: Plays a role in the flagellum-specific transport system 'I' SUBCELLUAR LOCATION: Integral membrane protein. Inner membrane. 'I MISCELLAMBOUS: For insertion of file into the membrane, cleavage of the signal peptide is important kinetically but not absolutely
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6 LRRLLRLLVLGIWLALLRSVAGEQAPG--TAP-CSRGSSWSADLDKCMDCASCRARP---
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Obnishi K., Fan F., Schoenhals G.J., Kihara M., Macnab R.M., "The Pilo, Filo, and Fila proteins of Salmonella typhimurium: putative components for flagellar assembly."; J. Bacteriol. 179:6092-6099(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FLAGELLAR BIOSYNTHETIC PROTEIN FLIP
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C9A4241F0653A4D4 CRC64;
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-!- SIMILARITY: BELONGS TO THE FLIP/MOPC/SPAP FAMILY.
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ID PORD METTH STANDARD;

AC P56815;

DT 30-MAY-2000 (Rel. 39, Created)
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Best Local Similarity 30.89,
These 33; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; L49021; AAB81319.1;
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108
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185 2
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245 AA;
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homeostasis
                                                                                                                                                                                                                                                                                                                                                                                                        A Smith D.R., Doucette-Gramm L.A., Deloughery C., Lee H.-M., Dubois J., Aldredge T., Bashizzadeh R., Blakely D., Cook R., Gilbert K., Harrison D., Hoang L., Keagle P., Lumm W., Pothier B., Qiu D., Badafora R., Vicare R., Wang Y., Wiezzbowski J., Gibbor R., Jiwani N., Caruso A., Bush D., Safer H., Patwell D., Prabhakar S., Mobugall S., Shime G., Goyal A., Pietrovski S., Church G.M., Daniels C.J., Mao J.-I., Rice P., Noelling J., Reeve J.N.; Recelet Genome sequence of Methanobacterium thermoautcotrophicum deltaH: functional analysis and comparative genomics."; J. Carling ACTIVITY: Pyruvate + CoA + oxidized ferredoxin = acetyl-COA + CO(2) + reduced ferredoxin.

C. -I CATALYTIC ACTIVITY: Pyruvate + CoA + oxidized ferredoxin = acetyl-COA + CO(2) + reduced ferredoxin.

C. -I CORDITY: HETEROTETRAMER OF ONE ALPHA, ONE BETA, ONE DELTA AND ONE GAMMA CHAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the EMDL outstation. The Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -1- SIMILARITY: BELONGS TO THE BACTERIAL TYPE FERREDOXIN FAMILY.
-1- CAUTION: THERE SEEMS TO BE A SEQUENCING ERROR THAT FUSES TOGETHER
PORC AND PORD. WE HAVE CUT THE ORF INTO ITS TWO CONSTITUENTS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     31 PGTAPCSRGSSWSA-----DLDKCMDCASCRA-----RPHS---DFCLGCA-AAPPA
30-MAY-2000 (Rel. 39, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Pyruvate synthase subunit porD (EC 1.2.7.1) (Pyruvate oxidoreductase
delta_chain)_(POR) (Pyruvic-ferredoxin oxidoreductase delta subunit).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21; Indels 17; Gaps
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Oxidoreductase; Electron transport; Iron-sulfur; Repeat; 4Fe-4S;
                                                                                                                                                          Methanobacterium thermoautotrophicum.
Archaea; Buryarchaeota; Methanobacteria; Methanobacteriales;
Methanobacteriaceae; Methanothermobacter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 73.5; DB 1; Length 81;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IRON-SULFUR 1 (4FE-4S) (180N-SULFUR 1 (4FE-4S) (180N-SULFUR 2 (4FE-4S) (180N-SULFUR 1 (4FE-4S) (180N-S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AE000929; AAB86210.1; ALT_INIT.
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PROSITE; PS00198; 4FE4S_FERREDOXIN;
                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=98037514; PubMed=9371463;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12.1%;
29.2%;
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Les 19; Conservative
                                                                                                                                                                                                                                                           NCBI_TaxID=187420;
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                                                                                                                            OR MTH1740.1.
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METAL 34
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MEDLINE=99452593; PubMed=10521297;
Millat G., Marcais C., Rafi M.A., Yamamoto T., Morris J.A.,
Millat G., Marcais C., Rafi M.A., Yamamoto T., Morris J.A.,
Pentchev P.G., Ohno K., Wenger D.A., Vanier T.;
"Niemann-Pick Cl disease: the 11061T substitution is a frequent mutant
allele in patients of Western European descent and correlates with a
classic juvenile phenotype.";
                                                                                                                                                                                                                                                                       Carstea B.D., Morris J.A., Coleman K.G., Loftus S.K., Zhang D., Cummings C., Gu J., Rosenfeld M.A., Pavan W.J., Krizman D.B., Wagle J., Polymeropoulos M.H., Sturley S.L., Ioannou Y.A., Higgins M.E., Comly M., Cooney A., Brown A., Kaneski C.R., Blanchette-Mackie E.J., Dwyer N.K., Neufeld E.B., Chang T.-Y., Liscum L., Strauss J.F. III, Ohno K., Zeigler M., Carmi R., Sokol J., Markie D., O'Neill R.R., van Diggelen O.P., Blleder M., Tagle D.A., Patterson M.C., Brady R.O., Vanier M.T., Pentchev P.G., Tagle D.A., Mineman.-Pick CI disease gene: homology to mediators of cholesterol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Watari H., Blanchette-Mackie B.J., Dwyer N.K., Glick J.M., Patel S., Neufeld B.B., Brady R.O., Pentchev P.G., Strauss J.F. III;
"Niemann-Pick CI protein: obligatory roles for N-terminal domains and lysosomal targeting in cholesterol mobilization.";
Proc. Natl. Acad. Sci. U.S.A. 96:805-810(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VARIANTS NPC1 GLN-934; LEU-940; ASN-948; LEU-954; TRP-992; ALA-1007; THR-1061 AND VAL-1213.
MEDLINE=99452586; PubMed=10521290;
Greer W.L., Dobson M.J., Girouard G.S., Byers D.M., Riddell D.C., Neumann P.E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Mutations in NPC1 highlight a conserved NPC1-specific cysteine-rich
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=98299797; PubMed=9634529; Greer W.L., Riddell D.C., Gillan T.L., Girouard G.S., Sparrow S.M., Byers D.M., Dobson M.J., Neumann P.E.; "The Nova Scotia (type D) form of Niemann-Pick disease is caused by G3097--- Transversion in NPC1.";
                                                                                                                                             Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "The genomic organization and polymorphism analysis of the human Niemann-Pick Cl gene.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
MEDLINES-1653216; PubMed=11754101;
MEDLINES-2163216; PubMed=11754101;
Bauer P., Knoblich R., Bauer C., Finckh U., Hufen A., Kropp J.,
Braun S., Kustermann-Kuhn B., Schmidt D., Harzer K., Rolfs A.;
"NPC1. Complete genomic sequence, mutation analysis, and
characterization of haplotypes.";
Hum. Mutat. 19:30-38(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Morris J.A., Zhang D., Coleman K.G., Nagle J., Pentchev P.G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Biochem. Biophys. Res. Commun. 261:493-498(1999).
                   Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                               SEQUENCE FROM N.A., AND VARIANTS NPC1.
MEDLINE=97362323; PubMed=9211849;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Am. J. Hum. Genet. 65:1252-1260(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A., AND VARIANTS.
MEDLINE=99355599; PubMed=10425213;
                                                                                  Niemann-Pick Cl protein precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CHARACTERIZATION.
MEDLINE=99128318; PubMed=9927649;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Am. J. Hum. Genet. 63:52-54 (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Science 277:228-231(1997).
                   30-MAY-2000 (Rel. 39, 30-MAY-2000 (Rel. 39, 15-SEP-2003 (Rel. 42,
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                                                                                                                            Homo sapiens (Human).
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                                                                                                                                                                                        NCBI_TaxID=9606;
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70

74 PFRLL 78 PVKAI 75

엄 ð 셤

71

1278 AA.

PRT;

STANDARD;

NPC1_HUMAN ID NPC1_HUMAN

RESULT 8

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Zhang H.,

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MEDLINE=99408226; PubMed=10480349;
Yamamoto T., Nanba E., Ninomiya H., Higaki K., Taniguchi M., Zhang H.,
Akaboshi S., Watanabe Y., Takeshima T., Inui K., Okada S., Tanaka A.,
Sakuragawa N., Millat G., Vanier M.T., Morris J.A., Pentchev P.G.,
                                                                                                                                                            MEDLINE=21313111; PubMed=11349231; Sun X., Marks D.L., Park W.D., Wheatley C.L., Puri V., O'Brien J.F., Kraft D.L., Lundquist P.A., Patterson M.C., Pagano R.E., Snow K.; Niemann-Pick C variant detection by altered sphingolipid trafficking and correlation with mutations within a specific domain of NPC1.", Am. J. Hum. Genet. 68:1361-1372(2001).
                                                                                                                                                                                                                                              VARIANTS NPC1 ALA-378; MET-950; ARG-992 AND THR-1061.
MEDLINE-21313105; PubMed=1133381;
Millat G., Marcais C., Tomasetto C., Chikh K., Fensom A.H., Harzer K.,
Wenger D.A., Ohno K., Vanier M.T.;
"Niemann-Pick C1 disease: correlations between NPC1 mutations, levels
of NPC1 protectin, and phenotypes emphasize the functional significance
of the putative sterol-sensing domain and of the cysteine-rich
                                                                                     Ohno K.;
"NPC1 gene mutations in Japanese patients with Niemann-Pick disease
                        VARIANTS NPC1, AND VARIANTS ARG-215; VAL-858 AND GLN-1266.
 Am. J. Hum. Genet. 65:1321-1329(1999).
                                                                                                                                                                                                                                                                                                                                              Am. J. Hum. Genet. 68:1373-1385(2001).
[11]
                                                                                                                                                 VARIANTS NPC1 GLN-958 AND ALA-1007.
                                                                                                                          Hum. Genet. 105:10-16(1999).
                                                                                                                                                                                                                                    10]
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MEDLINE=21372069; PubMed=11479732; Ribeiro I., Marcao A., Amaral O., Sa Miranda M.C., Vanier M.T., Millat G.; VARIANTS NPC1 TYR-177; CYS-978 AND VAL-1035.

"Niemann-Pick type C disease: NPC1 mutations associated with severe and mild cellular cholesterol trafficking alterations.",
Hum. Genet. 190:24-32 (2001).

-!-FUNCTION: INVOLVED IN THE INTRACELLULAR TRAFFICKING OF CHOLESTEROL. MAY PLAY A ROLE IN VESICULAR TRAFFICKING IN GLIA, A PROCESS THAT MAY BE CRUCTAL FOR MAINTAINING THE STRUCTURAL AND FUNCTIONAL INTEGRITY OF NERVE TERMINALS.

-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. FOUND IN LATE ENDOSOMES AND LYSOSOMES.

-!- DOMAIN: A CYSTEINE-RICH N-TERMINAL DOMAIN AND A C-TERMINAL DOMAIN CONTAINING A DI-LEUCINE MOTIF NECESSARY FOR LYSOSOME.

PTM: GLYCOSYLATED.

The Firm: Call Collects in NPC1 are the cause of Niemann-Pick disease

Type C1 (NPC1) [MIM.257220]; an autosomal recessive lipid storage disorder, which affects particularly the brain, liver and spleen, and which is characterized by lysosomal accumulation of low density lipoprotein derived cholesterol. Clinical features include variable hepatosplenomegaly and severe progressive neurological dysfunction such as ataxia, dystonia and dementia. The age of onset can vary from infancy to late adulthood.

-1- DISEASE: Defects in NPC1 are the cause of Niemann-Pick disease without sphingomyelinase deficiency, or Nova Scotian type. Because of evidence from biochemical changes, lack of complementation, and linkage mapping to the same chromosome site, NPD and NPC1 are considered to be allelic disorders.

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EMBL; AF002020; AAB63982.1; -. EMBL; AF157379; AAD48006.1; -.

FBN1_MOUSE STANDARD; FRT; 2871 AA. AC Q61584; Q60826; DT 01-NOV-1997 (Rel. 35, Last sequence update)

RESULT 9

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              33 TAPCSRGSSWSADLDKCMDCA-SCRARPHSDFCLGCAAAPPAAFRLLWPILG----GAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
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InterPro; IPR003392; Patched.
InterPro; IPR00031; SSD 5TW.
Pfam; PF02460; Patched; I.
IIGRPAMS; IIGR00917; 2A060601; 1.
PROSITE; PS50156; SSD; 1.
Signal; Glycoprotein; Transmembrane; Lysosome; Polymorphism;
                                                                                                                                                                                         MIM; 27220; -.
MIM; 257250; -.
GO; GO:0016021; C:integral to membrane; TAS.
GO; GO:0005764; C:lysosome; TAS.
GO; GO:0005764; C:lysosome; TAS.
GO; GO:0005248; E:intracellular transporter activity; TAS.
GO; GO:0015248; F:sterol transporter activity; TAS.
GO; GO:001888; F:transmembrane receptor activity; TAS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 72; DB 1; Length 1278;
                                                                                                                                                                                                                                                                                                                                                             POTENTIAL.
NIEMANN-PICK C1 PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                        DI-LEUCINE MOTIF.
                                                                                                                                                                                                                                                                                                                                                                                                                                 POTENTIAL.
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POTENTIAL.
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                                                                                                                  EMBL; AFIS, ...
EMBL; AFIS7378; AAD4ev...
EMBL; AF338230; AAK28791.1; -..
R EMBL; AF123046; AAF28875.1; -..
R EMBL; AF123045; AAF28875.1; JOINED.
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AAD48006.1;
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11145
11145
1216
1248
122
122
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                              AF157368;
AF157369;
                                                                                          AF157374;
AF157375;
AF157376;
AF157377;
            157366;
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CARBOHYD
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EMBL;
EMBL;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FACH" N.A.
STRAIN=CD-1; TISSUE=Kidney;
OCA K., Kumar A., Wada J., Liu Z., Kanwar Y.S.;
OCA K., Kumar A., Wada J., Liu Z., Kanwar Y.S.;
Submitted (APR-1995) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: STRUCTURAL COMPONENT OF CONNECTIVE TISSUE MICROFIBRILS
THAT BINDS CALCIUM. FIBRILLIN-1-CONTAINING MICROFIBRILS PROVIDE
-!- PIN: FORM FORCE BEARING STRUCTURAL SUPPORT.
-!- PIN: FORMS INTERNOLECULAR DISULFIDE BONDS EITHER WITH OTHER
FIBRILLIN-1 MOLECTULES OR WITH OTHER COMPONENTS OF THE
MICROFIBRILS (BY SIMILARITY)
-!- SIMILARITY: Contains 47 EGF-like domains.
-!- SIMILARITY: Contains 7 TGF-beta binding protein (TGFBP) domains.
                                                                                                                              MEDLINE=95130561; PubMed=7829516;

Yin W., Germiller J., Sanguineti C., Smiley E., Pangilinan T.,

Yin W., Ramirez F., Bonadio J.;

"Primary structure and developmental expression of Fbn-1, the mouse fibrillin gene.";

J. Biol. Chem. 270:1798-1806(1995).

[2]

SEQUENCE FROM N.A.
                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
28-FEB-2003 (Rel. 41, Last annotation update)
Fibrillin 1 precursor.
FBN1 OR FBN-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL, L29454; AAA56840.1; -. EMBL, U22493; AAA64217.1; -. PIR; A55524. A55524. HSSP, P35555; 1APJ. MGD; MGI:95489; Fbnl.
                                                Mus musculus (Mouse)
                                                                                                     NCBI_TaxID=10090
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BGF-CONTAINING FIBULIN-LIKE EXTRACELLULAR MATRIX PROTEIN 2.
BGF-LIKE 1, DIVERGENT.
BGF-LIKE 2, CALCIUM-BINDING (POTENTIAL).
BGF-LIKE 3, CALCIUM-BINDING (POTENTIAL).
BGF-LIKE 5, CALCIUM-BINDING (POTENTIAL).
BGF-LIKE 6, CALCIUM-BINDING (POTENTIAL).
BGF-LIKE 6, CALCIUM-BINDING (POTENTIAL).
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           Mus musculus (Mouse).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                               Gallagher W.M., Argentini M., Sierra V., Bracco L., Debussche L.,
                                                                                                                     "MBP1: a novel mutant p53-specific protein partner with oncogenic properties.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BY SIMILARITY.
N-LINKED (GLCNAC. . .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                PROSITE; PS00010; ASX HYDROXYL; 4.
PROSITE; PS00022; EGF_1; FALSE_NEG.
PROSITE; PS01186; EGF_2; 4.
PROSITE; PS01187; EGF_CA; 6.
Repeat; EGF-1ike domain; Calcium-binding; Glycoprotein; Signal.
SIGNAL
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Pred. No. 13;
5; Mismatches 33; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4969C0328A23DD88 CRC64;
                                                                                                                                        Oncogene 18:3608-3616(1999).
-!- SUBUNIT: BINDS PREFERENTIALLY TO P53 MUTANTS.
-!- SUBCELLULAR LOCATION: Secreted.
-!- SIMILARITY: Belongs to the fibulin family.
-!- SIMILARITY: Contains 6 EGF-like domains.
                                                                         STRAIN=C57BL/6J;
MEDLINE=99308589; PubMed=10380882;
                                                                                                                                                                                                                                                                                                    HSSP, P00736; IAPQ.
MGD; MGI:1891209; Efemp2.
InterPro; IPR001152; Asx. hydroxyl.
InterPro; IPR001881; EGF.Ca.
InterPro; IPR001891; EGF.Tike.
InterPro; IPR001491; Thrmbomoduln.
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PRINTS; PR00907; THRMBOMODULN.
SMART; SMO0179; EGF_CA; 4.
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  EFEMP2 OR FBLN4 OR MBP1.
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16-0CT-2001 (Rel. 40, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
EGF-containing fibulin-like extracellular matrix protein 2 precursor (Fibulin-4) (FIBL-4) (Mutant p53 binding protein 1).
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N-LINKED (GLCNAC. .) (POTENTIAL).
O-LINKED (GLYCOSAMINOGLYCAN) (POTENTIAL).
O-LINKED (GLYCOSAMINOGLYCAN) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  in the adult rat nervous system.";
J. Neurosci. 14:3713-3724(1994).
-!- FUNCTION: CELL SURFACE PROTEOGLYCAN THAT BEARS HEPARAN SULFATE.
MAY PLAY AN IMPORTANT ROLE IN THE TROPHIC AND INJURY RESPONSES OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor.
-!- TISSUE SPECIFICITY: NERVOUS SYSTEM.
-!- PTM: THIS CELL-ASSOCIATED GLYDICAN IS FURTHER PROCESSED TO GIVE
RISE TO A MEDIUM-RELEASED SPECIES.
-!- SIMILARITY: Belongs to the glypican family.
                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE=Brain;
MEDLINE=93038690; PubMed=1417860;
Karthikeyan L., Maurel P., Rauch U., Margolis R.K., Margolis R.U.;
"Clothikeyan L. anjor heparan sulfate proteoglycan from brain and identification as the rat form of glypican.";
Biochem. Biophys. Res. Commun. 188:395-401(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Litwack E.D., Stipp C.S., Kumbasar A., Lander A.D., "Neuronal expression of glypican, a cell-surface glycosylphosphatidylinositol-anchored heparan sulfate proteoglycan,
      LVLGLWLALLRSVAGEQAP----GTAPCSRGSSWSADLDKCMDCASCRARPHS----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A., AND SEQUENCE OF 83-112; 196-207 AND 422-443.
STRAIN=New England Deaconess Hospital;
MEDLINE=94267529; PubMed=8207484;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Proteoglycan, Heparan sulfate; Glycoprotein, Signal, GPI-anchor;
Extracellular matrix.
                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A., AND SEQUENCE OF 24-55 AND 424-445.
                                                                                                                                                                                                                   01-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
08-FEB-2003 (Rel. 41, Last annotation update)
01_Ypican-1 precursor (HSPG MI2).
                                                                                                                                                                                         558 AA
                                                                      -----DFCLGCAAA------PPAP 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GLYPICAN-1
                                                                                                   72 INHYGGYLCLPRSAAVISDLHGEGPPPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; I34067; AAA41251.1; -.
PIR; I56545; I56545.
InterPro; IPR001863; Glypican.
Pfam; PF01153; Glypican; I.
PROSITE; PS01207; GLYPICAN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; L02896; AAA86439.1; -.
                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                    Rattus norvegicus (Rat)
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538
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79
116
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                                     12
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                                                                                                                                                                                    GPC1 RAT
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CARBOHYD
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                                                                                                                                                                                                                                                                                                64
  (GLYCOSAMINOGLYCAN) (POTENTIAL). (GLYCOSAMINOGLYCAN) (POTENTIAL).
                                                                                                                                                                                                                                                                                      11 RLLVLGLWLA--LLRSVAGEQAPGTAPCSRGSSWSADLDKCMDCASCR----ARPHSDFC
                                                                                                                                                                                                                                                       Gaps
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SECURING B.B., Renfranz P.J., Lilly B., Beckerle M.C.,
"Muscle LIM proteins associate with muscle sarcomeres and require
dMEF2 for their expression during brosophila myogenesis.";
Submitted (SEP-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Drosophila melanogaster (Fruit fly).

Eukaryota, Metazoa, Arthropoda, Hexapoda; Insecta, Pterygota, Mosptera, Endopterayota, Diptera, Brachycera, Muscomorpha, Ephydroidea, Drosophilidae, Drosophila.
                                    21 T -> A (IN REF. 2).
312 Y -> N (IN REF. 2).
437 I -> G (IN REF. 2).
443 E -> D (IN REF. 2; AA SEQUENCE)
515 I -> T (IN REF. 2; AA SEQUENCE)
61734 WW; E2878A854B9AID7F CRC64;
                                                                                                                                                                                                        Score 70; DB 1; Length 558;
Pred. No. 16;
6; Mismatches 19; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Stronach B.E., Siegrist S.E., Beckerle M.C.; "Two muscle-specific LIM proteins in Drosophila."; J. Cell Biol. 134:1179-1195(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q24400; Q9VI62;
01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
Muscle LIM protein MLP84B.
LIM3 CR MLP84B OR CG10699.
                         O-LINKED
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MEDLINE=96387325; PubMed=8794860;
                                                                                                                                                                                                        th
| Similarity 37.7%;
| Conservative
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RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
Rak Liu X., Mattei B., McIntosh T.C., McLeod M.P., McDherson D.,
Rak Liu X., Mattei B., McIntosh T.C., McLeod M.P., McDherson D.,
Rekriov G., Milshina N.V., Mobary C., Morris J., Moshrefi A.,
Rak Mcunt S.M., Moy M., Murphy B., Murphy D.M., Nalson D.L.,
Rak Relazzlo M., Pittman N.V., Nabary C., Morris J.D.M., Nalson D.L.,
Rak Relazzlo M., Pittman G.S., Pan S., Pollard J., Puri V., Reses M. G.,
Rak Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
Spier B.C., Siden-Kiamos I., Simpson M., Stupski M.P., Smith T.,
Rak Spier B., Spradling A.C., Stapleton M., Stupski M.P., Smith T.,
Rak Spier B., Spradling A.C., Stapleton M., Stupski M.P., Smith T.,
Ray Spier B., Spradling A.C., Stapleton M., Stupski M.P., Smith T.,
Ray Spier B., Modage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
Ray Milliams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
Ray Zheng X.H., Zhong F.M., Zhong W., Zhou X., Zhang G., Zhao Q., Zheng I.,
Ray Zheng X.H., Zhong F.M., Zhong W., Zhou X., Zhan S., San X., Smith H.O.,
Ray Zheng X.H., Mores E.W., Kubin G.M., Venter J.C.,
R. Zheng X.H., Mores E.W., Kubin G.M., Venter J.C.,
R. Zheng X.H., Mores E.W., Kubin G.M., Venter J.C.,
R. Zhong F.M., Mores E.W., Mores E.W., Smith H.O.,
R. Science 287:2185-2195(2000)
C. - FUNCTION: PLANS A ROLL IN THE EMBRYO, EXPRESSION IS RESTRICTED TO THE SOMATIC, VICERAL, AND PHARNMEAL MYSCIES. WITHIN THE SOMATIC
C. - FUNCTION: PLANS A ROLL IN THE EMBRYO, EXPRESSION IS RESTRICTED TO THE PIDERMI THE MUSCULATURE IS DIFFRENTIATION. WHEN THE MUSCULE WITHIN THE SOUND TO THE PIDERMI THE MUSCULATURE IS DIFFRENTIATION.
C. - FUNCTION: WHEN THE MUSCULE WITHING IN EVERDERS THE ENDING WHEN THE MUSCULATURE IS DIFFRENTIATION.
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C. STMILARITY: TO THE WISCILE PRE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Fram; PR00412; LIM; S.
ProDom; PB000094; LIM; S.
SMARI; SM00132; LIM; D.
PROSITE; PS00478; LIM DOMAIN 1; S.
PROSITE; PS50023; LIM DOMAIN 2; S.
Nuclear protein; Repeat; LIM domain; Metal-binding; Zinc; Myogenesis; Developmental protein; Differentiation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GLY-RICH.
NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
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LIM 3.
GLY-RICH.
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LIM 5.
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EMBL; AF090832; AAC61591.1; -.
EMBL; AE003672; AAF54063.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HSSP; P32965; 1CTL.
FlyBase; FBgn0014863; Mlp84B.
InterPro; IPR001781; LIM.
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1120
1175
1178
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495 AA;
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Gaps

15;

37; Indels

11.4%; Score 69.5; DB 1; Length 495; 28.0%; Pred. No. 16; ive 7; Mismatches 37; Indels 19

23; Conservative

Query Match Best Local Similarity Matches 23; Conserv

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110 AIARAPEGEGCPRCGGYVYAAAEQMLARGRSWHKECFKCGTCKKGLDSILCCEAPDKNIYC 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WEDLINE-20288799; PubMed=10830953;
WIEDLINE-20288799; PubMed=10830953;
WIEDLINE-20288799; PubMed=10830953;
WIEDLINE-20288799; PubMed=10830953;
WIEDLINE-20288799; PubMed=10. Taylor T.D., Watanabe H., Yada T.,
WA Bark H.-S., Toydad A., Ishli K., Totcki Y., Choi D.-K., Groner Y.,
WA Soeda E., Ohki M., Takagi T., Sakaki Y., Taudien S., Blechschmidt K.,
WA Colley A., Menzel U., Delabar J., Kumpf K., Lehmann R., Patterson D.,
Rosenthal A., Kudoh J., Shillabel M., Schudy A., Zimmermann W.,
WA Shintani A., Sasaki T., Nagamine K., Mitsuyama S., Antonarakis S.E.,
Minoshima S., Shimizu N., Nordsiek G., Hornischer K., Brandt P.,
Wanneshim S., Shimizu N., Nordsiek G., Hornischer K., Broner G.,
Wannest J., Beck A., Klages S., Hennig S., Riesselmann L., Dagand E.,
Wehrmeyer S., Borzym K., Gardiner K., Nizetic D., Francis F.,
Wature 405:311-319(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUB=Colon, Lung, Muscle, and Ovary;

X MEDLINE=22388257, PubMed=12477932,

X Stausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

XA Altasner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

XA Altschul S.F., Zeeberg B., Butcow K.H., Schefer C.F., Bhat N.K.,

A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Brownstein M.J., Uddin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Brownstein M.J., Uddin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P. H.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
20 ALLRSVAGEQAP-----GTAPCSRGSSWSADLDKCMDCAS-----CRARPHSDFC 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Cloning of a novel human putative type Ia integral membrane protein mapping to 21922.3.";
                                                                                                                                                                                                                                                    PTTG HUMAN STANDARD; PRT; 180 AA.

101-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
01-0CT-1996 (Rel. 34, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Pituitary tumor-transforming gene 1 protein-interacting protein
Pituitary tumor-transforming gene protein binding factor) (Pituitary tumor-transforming gene protein binding factor) (PTTG-1P OR CZIORFI OR CZIORFI)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A., CHARACTERIZATION, AND INTERACTION WITH PTTG1.
MEDLINE-20317150; PubMed=10781616;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chien W., Pei L., "A novel binding factor facilitates nuclear translocation and transcriptional activation function of the pituitary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Yaspo M.-L., Aaltonen J., Horelli-Kuitunen N., Peltonen L.,
Lehrach H.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              tumor-transforming gene product.";
J. Biol. Chem. 275:19422-19427(2000).
                                                                                                                                       170 KGCYAKKFGPKGYGYGQGGGAL 191
                                                                                                98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=98234553; PubMed=9570958;
                                                                                           65 LGCAAAPPAPFRLLWPILGGAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Genomics 49:133-136(1998).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        67 CAAAPPAP-----FRLLW-----PILGGALSLTFVLGLLSGFLVWRRCRRER 108
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        Sanchez A.,
                                                                                                                                                                          -!- SUBCELLULAR LOCATION: According to Ref.2, it is found in the cytoplasm and in the nucleus. According to Ref.1, it is a type I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                POLY-CYS,
PTPYWRLRIGG -> ARRIGGCASV (IN REF. 2).
Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.M., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.; Gleeration and initial analysis of more than 15,000 full-length human and mouse cDNA sequences."; Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (IN REF. 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 180;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                43; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TLLLGIA -> NPPPGHC (IN REF
F1E66014D49EC1DE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GO; GO:0006606; P:protein-nucleus import; IDA.
InterPro; IPR003659; Plexin-like.
SMART; SM00423; PSI; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              014140;
15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Hypothetical protein KIAA0127.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 Similarity 25.8%; Pred. No. 7; 32; Conservative 19; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         314 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11.3%; Score 69;
                                                                                                                                                                                                              membrane protein.
-!- TISSUE SPECIFICITY: Ubiquitous.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                          -!- SUBUNIT: Interacts with PTTG1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GO; GO:0005737; C:cytoplasm; IDA.
GO; GO:0005634; C:nucleus; IDA.
                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AF149785; AAF73770.1; --
EMBL; AL163300; CAB90552.1; --
EMBL; BC000415; AAH00415.1; --
EMBL; BC012285; AAH12285.1; --
EMBL; BC012295; AAH12295.1; --
EMBL; BC020983; AAH20983.1; --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nuclear protein.
17 117 POT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GO:0005634; C:nucleus; IDA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HGNC:13524; PTTG1IP.
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Best Local
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Y127 HUMAN
AC Q14140;
DT 15-JUL.
DT 28-FEB-
DE HYPOTHE
GN KIAA012
GN HOMO 95
OC BUKATY
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@ib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ij
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               inducing signaling complex (DISC) performs caspase-8 protectly activation which initiates the subsequent cascade of cappases (aspartate-specific cysteine proteases) mediating apoptosis. FAS-mediated apoptosis may have a role in the induction of peripheral tolerance, in the antigen-stimulated suicide of mature T-cells, or both (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Biochem. Biophys. Res. Commun. 198:666-674(1994).
-1- FUNCTION: Receptor for TNPSF6/FASL. The adaptor molecule FADD
recruits caspase-8 to the activated receptor. The resulting death-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TNFRSF6 OR PT1 OR FAS.
Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                           Nagase T., Seki N., Tanaka A., Ishikawa K.-I., Nomura N.,
"Prediction of the coding sequences of unidentified human genes. IV.
The coding sequences of 40 new genes (KIAA0121-KIAA0160) deduced by
analysis of cDNA clones from human cell line KG-I.",
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -!- SUBUNIT: Binds DAXX and ALENA NOT CONTROL Protein.
-!- SUBCELLULAR LOCATION: Type I membrane protein.
-!- DOMAIN: CONTAINS A DEATH DOMAIN INVOLVED IN THE BINDING OF FADD,
AND MAYBE TO OTHER CYTOSOLIC ADAPTOR PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=Sprague-Dawley, TISSUE=Liver;
MEDI:TNE=94128114, PubMed=7507668,
Kimura K., Yamamoto M., Wakatsuki T.,
"A variant mRNA species encoding a truncated form of Fas antigen in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   precursor (FASL (Apo-1 antigen)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30 APGTAPCSRGSSWSADLDKCMDCASCRARPHSDFCLGCAAAPPAPFRLLWPIL 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2,
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 1; Length 314;
12;
                                                                                                                                                                                                                                                                                                                                                                                                                             314 AA; 33896 MW; E43107FC565AAC31 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15-JUL-1999 (Rel. 38, Last sequence update)
LSSP-2003 (Rel. 42, Last annotation update)
Tumor necrosis factor receptor superfamily member 6
receptor) (Apoptosis-mediating surface antigen FAS)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- SIMILARITY: Contains 3 TNFR-Cys repeats.
-!- SIMILARITY: Contains 1 death domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 69;
Pred. No.
                                                                          TISSUE=Bone marrow;
MEDLINE=96127530; PubMed=8590280;
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15-JUL-1999 (Rel. 38, Last seq
15-SEP-2003 (Rel. 42, Last ann
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34.0%;
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                                                      FROM N.A.
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                  NCBI TaxID=9606;
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Biochem. Biophys.
                                                                                                                                                                                                                                                                                                                                                                                                      Hypothetical
                                                        SEQUENCE
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                                                                                                                                          R BMBL; D26112; BAA05108.1; -
R PIR; JC2395; JC2395.
R HSSP; P25445; 1DDF.
R InterPro; IPR001368; Dath.
InterPro; IPR001368; TWFR c6.
R Pfam; PF00020; TWFR c6; 3.
SMART; SM00005; DEATH; 1.
R SMART; SM00065; DEATH; 1.
R PROSITE; PS00652; TWFR MGFR 1; 2.
R RPOSITE; PS00650; TWFR MGFR 2; 2.
R R PROSITE; PS00007; DEATH DOMAIN; 1.
R PROSITE; PS00017; DEATH DOMAIN; 1.
R PROSITE; PS000
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N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
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SUPERFAMILY MEMBER 6.
POTENTIAL.
CYTOPLASMIC (POTENTIAL).
TYRR-CYS 1.
TYRR-CYS 2.
TYRR-CYS 2.
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Best Local Similarity 18.2%; Pred. No. 12;
Matches 24; Conservative 18; Mismatches 34; Indels
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D25D583C909D9D09 CRC64;
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324 AA;
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172
189
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Search completed: February 11, 2004, 10:38:33 Job time : 15 secs

101 WRRCRRERSSPP 112 ::| |: : | 188 YKRYRKRQPGDP 199

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30 APGTAPCSRGSSWSAD---LDKCMDCA------60

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Q8v370 mus musculu
Q8bmi5 mus musculu
Q8bzr3 salmonella
Q9qee6 indian citr
O53668 mycobacteri
O18288 caenorhabdi
Q96kn9 homo sapien
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Q9a9x4 caulobacter
Q8k406 mus musculu
P90890 caenorhabdi
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09n0b3 macaca fasc
042839 hordeum vul
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Q9bzg2 homo sapien
                                                          February 11, 2004, 10:35:58; Search time 34 Seconds (without alignments) 865.235 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Listing first 45 summaries
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Q9N0B3
Q42839
Q8VD70
Q8BMI5
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Match Length DB
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Q9p2p7 homo sapien 004393 hordeum vul Q8pqd6 xanthomonas Q8n2r7 homo sapien	cyprin	Q9iar7 gallus gall Q8i8v6 giardia lam Q85054 homo sapien Q8w393 oryza sativ O93072 hepatitis g Q9631 baboon herp Q98255 streptomyce Q98100 rhizobium 1	QBTZ14 mus musculu QBTZ14 oryza sativ QBD347 xanthomonas QBTGa1 streptomyce Q95ca1 streptomyce Q95ca9 rhizobium m Q961p0 homo sapien QBTG37 human immun QBQG9 xanthomonas Q9tti0 sus scrofa Q9tja2 homo sapien
5 12.1 730 4 Q9P2P7 3 12.0 227 10 004393 3 12.0 243 16 Q8PQD6 3 12.0 370 4 Q8PXR7 3 12.0 768 13 009TU6	11.9 206 4 5 0 11.9 32.9 4 0 0 11.9 36.5 4 0 0 11.9 36.5 4 0 0 11.9 36.5 4 0 0 11.9 36.5 4 0 0 0 11.9 36.5 4 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	2 11.8 368 13 Q9IAR7 5 11.8 721 4 O95054 5 11.8 210 4 O95054 5 11.8 273 12 O93072 1 11.7 116 12 O9631 1 11.7 473 16 Q9S255 1 11.7 475 16 Q9S255 1 11.7 557 11 O90757	11.7 646 10 11.6 204 16 11.6 467 16 11.5 127 4 () 11.5 206 15 11.5 293 6 ()
17 73.5 18 73 19 73 20 73 21 73	22 23 24 25 25 25 26 26 27 20 20 20 20 20 20 20 20 20 20 20 20 20	0	7007

ALIGNMENTS

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                                                                                                                                                                                                                                                                 MEDLINE-21309073; PubMed=11414767;

Yousef G.M., Diamandis M., Jung K., Diamandis E.P.;

Yousef G.M., Diamandis M., Jung K., Diamandis E.P.;

Yousef G.M., Diamandis M., Jung K., Diamandis E.P.;

'Molecular cloning of a novel human acid phosphatase gene (ACPT) that is highly expressed in the testis.";

Genomics 74:385-395 (2001).

EMBL; AP321918 P. AAK09396.1; -.

InterPro; IPR000560; HisAc_phsphtse.

Fram; PF00328, acid phosphat; 1.

PROSITE; PS00616; HIS_ACID_PHOSPHAT_2; 1.

PROSITE; PS00616; HIS_ACID_PHOSPHAT_2; 1.

PROSITE; PS00778; HIS_ACID_PHOSPHAT_2; 1.

SEQUENCE 333 AA; 35402 Mw; 0CO237096567B30F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 31 PG-TAPCSRGSSWSADLDKCMDCASCRARPHSDFCLGC--AAAPPAPFRLLWPILGGALS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14; Gaps
                                                                                                                                                                              Bukaryota; Metazoa; Chordata, Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14.3%; Score 87; DB 4; Length 333; 35.3%; Pred. No. 0.45; tive 6; Mismatches 35; Indels
                                                                                                              Last annotation update)
                                                                                             Last sequence update)
                                         333 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       88 LTFVLGLLSGFLVWR-RCRRERSSP 111
                                                                             Created)
                                       PRT;
                                                                     01-JUN-2001 (TrEMBLrel. 17,
01-JUN-2001 (TrEMBLrel. 17,
01-MAR-2003 (TrEMBLrel. 23,
Acid phosphatase variant 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30; Conservative
                                     PRELIMINARY;
                                                                                                                                                                 (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                    NCBI_TaxID=9606;
                                                                                                                                                                 Homo sapiens
                                     Q9BZG3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
RESULT 1
Q9BZG3
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308 VLVALSLGLGLLAWRPGCLRALGGP 332

d

4;

Gaps

63

RESULT 2

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143 --NVPASPPPRISLSPPPPPSTPTQSGASSGSKSSNNGTVVAVGVAVAAVVVLGLAAGL 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ----RPPCTGVVDCY 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9 LLRLLVIGLWLALLRSVAGEQAPGTAPCSRGSSWSADLDKCMDCASCRARPHSDFCLGCA 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 libraries.";
Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
-!- FONTION ONE GAP JUNCTION CONSISTS OF A CLUSTER OF CLOSELY PACKED
-!- FAIRT OF TRANSMEMBRANE CHANNELS, THE CONNEXONS, THROUGH WHICH
MATERIALS OF LOW MW DIFFUSE FROM ONE CELL TO A NEIGHBORING CELL
                                                                                                                                                                                                                                         -CASCRARPHSDF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
Osada N., Hida M., Kusuda J., Tanuma R., Iseki K., Hirai M., Terao K.,
Suzuki Y., Sugano S., Hashimoto K.;
"Isolation of full-length cDNA clones from macaque brain cDNA
                                                                                                                                                                                                                                                                                                       ------ILGGALSLTFVLGLLSG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels 20; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIMILARITY)
-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY)
-!- SIMILARITY: BELONGS TO THE CONNEXIN FAMILY.
EMBL; AB046017; BAB01599-1; --
InterPro; IPR000500; Connexin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-0CT-2002 (TrEMBLrel. 22, Last annotation update)
Undamed protein product (Gap junction protein) (Connexin).
Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (BY SIMILARITY).
-!- SUBUNIT: A CONNEXON IS COMPOSED OF A HEXAMER OF CONNEXINS (BY
PROSITE; PS50011; PROTEIN KINASE DOM; 1.
PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
ATP-binding; Kinase; Receptor; Serine/threonine-protein kinase;
                                                                                                                                                                         57;
                                                                                                                                    610;
                                                                                                                                                                         35; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 341;
                                                                                                                                    Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    69 AAPPAPFRLLWPILGGALSLTFVLGLLSGFLVWRRCRRERSSPP 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 610 AA; 64405 MW; 2A7B3EBE83FA9303 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       341 AA; 36784 MW; 4A71DEA938F0FA0C CRC64;
                                                                                                                         Query Match
13.7%; Score 83.5; DB 10;
Best Local Similarity 24.6%; Pred. No. 1.8;
Matches 34; Conservative 12; Mismatches 35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   341 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
13.0%; Score 79; DB (Best Local Similarity 27.9%; Pred. No. 3.1; Matches 29; Conservative 9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                               30 APGTAPCSRGSSWSADLDKCMD--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PERMYS; PRO0029; CONDEXIN; 1.
SMART; SMO0037; CNX; 1.
PROSITE; PSO0407; CONNEXINS 1; 1.
PROSITE; PSO0408; CONNEXINS 1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                            | | :| || : |||
201 IYFFVSKRRRRRQHPPPP 218
                                                                                                                                                                                                                                                                                                                                                                                98 --FLVWRRCRRERSSPPP 113
                                                                                                                                                                                                                                                                                                  64 CLGCAAAPPAPFRLLWP----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gap junction; Transmembrane. SEQUENCE 341 AA; 36784 MW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cercopithecinae; Macaca.
NCBI_TaxID=9541;
                                                             Transferase
                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q9N0B3
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Q9N0B3
      8 4 4 5 5 S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      351 PGCPAPCPLGRFYQL-----TAPARPPAHGVSCHGPYEAAIPPAP---VVPLLAGAVA 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               31 PG-TAPCSRGSSWSADLDKCMDCASCRARPHSDFCLGC--AAAPPAAFRLLWPILGGALS 87
                                                                                                                                                                                                                                                                                                  [1] -
SEQUENCE FROM N.A.
MEDLINE=21309073; PubMed=11414767;
Yousef G.M., Diamandis M., Jung K., Diamandis B.P.;
Molecular cloning of a novel human acid phosphatase gene (ACPT) that
"Molecular cloning of the testis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae,
Ehrhartoideae, Oryzeae, Oryza.
                                                                                                                                                                                                                                         Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=cv. Nipponbare;
Sasaki T., Matsumoto T., Yamamoto K.;
Sasaki T., Matsumoto T., Yamamoto K.;
Cioryaa sastiva nipponbare(GA3) genomic DNA, chromosome 1, PAC
clone: P0046ED5.";
Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
-! SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
EMBL; AP003237; BAB67905.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cn 14.3%; Score 87; DB 4; Length 426; I Similarity 35.3%; Pred. No. 0.57; 30; Conservative 6: Mismatch...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR000560; Hishc phsphtse.
Pfam; PF00328; acid phosphat; 1.
PROSITE; PS00616; HIS ACID PHOSPHAT 1; 1.
PROSITE; PS00778; HIS ACID PHOSPHAT 2; 1.
SEQUENCE 426 AA; 46089 WW; BE930398041DB061 CRC64;
                                                                                                                                        Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Putative receptor protein kinase.
                                                                             426 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      610 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gramene; Q943GB; -.
InterPro; IRR000719; Prot kinase.
InterPro; IPR002290; Ser thr pkinase.
Pfam; PP00069; pkinase; 1.
ProDom; PD000001; Prot kinase; 1.
PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        401 VLVALSLGLGLLAWRPGCLRALGGP 425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     88 LTFVLGLLSGFLVWR-RCRRERSSP 111
                                                                                                                                                                                                                                                                                                                                                                                                          is highly expressed in the testis.", Genomics 74:385-395(2001).
EMBL: AF321918; AAK09393.1; -.
HSSP: P15309; 2HPA.
Genew; HGNC:14376; ACPT.
                                                                                                                       Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                         01-JUN-2001 (TrEMBLrel. 17,
01-JUN-2001 (TrEMBLrel. 17,
01-MAR-2003 (TrEMBLrel. 23,
                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                   Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Oryza sativa (Rice).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
                                                                                                                                                                              Acid phosphatase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                               NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=4530;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             P0046E05.12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                    Q9BZG2
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Best Loca Matches

0943G8

RESULT 3 Q943G8

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13 LVLGLWLALLRSV----AGEQAPG-TAP----CSRGSSWSADLDKCMDCASCRARPHSDF 63
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13 IVLSAALAMAMVKRAQQCGSQAGGATCPNCLCCSRFGYCGSTSDYC--GAGCQSQ----
                                                                                                                                                       Hordeum vulgare (Barley).
Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooldeae;
NCBI_TaxID=4513;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23; Gaps
                                                                                                                                                                                                                                                                                                                                           Tidentification of an enhancer/silencer sequence directing the aleurone-specific expression of a barley chitinase gene.";

Plant J. 6:579-589(1994).

REMBL; 134211; AAA67871.1.

RESP; P23951, 2BAA.

RINEPPRO; IPRO01022, Chitin binding 1.

REPRO; IPRO01022, Chitin binding 1.

Pfam; PF00187; Glyco hydro 19, 1.

Pfam; PF00187; Glyco hydro 19, 1.

Probom; PD00609; Chitin binding 1; 1.

Probom; PD000609; Chitin binding 1; 1.

RODOM; PD00070; Glyco hydro 19; 1.

ROSOMIE; RO00773; CHITINASE 19 1; 1.

ROSITE; RS00773; CHITINASE 19 1; 1.

ROSITE; RS00773; CHITINASE 19 1; 1.

ROSITE; RS00774; CHITINASE 19 2; 1.

ROSITE; RS00774; CHITINASE 19 1; 1.

ROSITE; RS00774; CHITINASE 19 2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE-Seed;
MEDLINE=95078949; PubMed=7987416;
Leah R., Skriver K., Knudsen S., Ruud-Hansen J., Raikhel N.V.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ch 12.9%; Score 78.5; DB 10; Length 332; l Similarity 32.0%; Pred. No. 3.4; 3.4; 33; Conservative 9; Mismatches 38; Indels 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              64 CLGCAAAPPAPFRLLWPILGGALSLTFVLGLLSGFLVWR-RCR 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CSGCGPTPPGPSP----GGGVSSIISRDLFEQFLLHRDRCQ 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
TISSUB-Salivary gland;
Strausberg R.;
Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC017526; AAH17526.1;
MGD; MGI:1934667; Infrsf25.
                                                                                         Last sequence update)
Last annotation update)
                                      332 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          387 AA
                                                                        Created)
                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                       (TrEMBLrel. 01, (TrEMBLrel. 23,
                                                                 01-NOV-1996 (TrEMBLrel. 01, 01-NOV-1996 (TrEMBLrel. 01, 01-MAR-2003 (TrEMBLrel. 23,
                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                    Chitinase (EC 3.2.1.14)
CHI33.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus (Mouse)
                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=10090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                              Q42839
Q42839;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        08VD70;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q8VD70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Loca
Matches
RESULT 5
Q42839
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 6
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138 GWCVDCSTEPCGKSSPFSCVPCGATTPVHEAPTPLFW--VQVLLGVAFLFGALLICAYCR 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4;
                                                                                                                                                                                                                                                                                               ------3A 30
                                                                                                                                                                                                                                                                                                                            77
                                                                                                                                                                                                                                                                                                                                                           61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99 LAGLRQOSLDKPCEASPCLNGGTCRVASGIFEC----TCSAGFSGQFCEVVKTLFLPLPFF 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19 IALLRSVAGEQAPGTAPCSRGSSW--SADLDXCMDCASCRARPHSDFCLGCAAAP-PAPF 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                [1]
SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STRAIN=C57BL/60; TISSUE=Forelimb;
MEDLINE=2234683; PubMed=12466851;
The FANTOM Consortium,
The RANTOM Consortium,
The RIKEN Genome Exploration Research Group Phase I & II Team;
"Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs.";
Nature 420:563-573(2002).
Nature 420:563-573(2022).
NATURE 420:563-573(2022).
                                                                                                                                                                                                                                                                                                          31 PGTAPC-----ASCRARPLDENCMDC-----ASCRARP----HS
                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                               85;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q8BMIS, PRELIMINARY; PRT; 219 AA.
Q8BMIS;
01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Weakly similar to neurogenic locus notch 3 protein (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6
                                                                                                                                                                                                                        Query Match 12.9%; Score 78.5; DB 11; Length 387; Best Local Similarity 18.9%; Pred. No. 3.9; Matches 35; Conservative 21; Mismatches 44; Indels 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 30.0%; Pred. No. 2.9;
Matches 30; Conservative 16; Mismatches 45; Indels 9,
                                                                                                                                                                                            41640 MW; F16644666BAD68D3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQÜENCE 219 AA; 23098 MW; 9F2C4BE237F9B522 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 76 RLLWPILGGALS--LTFVLGLLSGFLVWRRCRRERSSPPP 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4 GSLRRLLRLLVLGLWLALLRSVAGE----
InterPro; IPR000488; Death.
InterPro; IPR005209; EGF like.
InterPro; IPR001368; TNFR_c6.
Pfam; PF00531; death; 1.
Pfam; PF00020; TNFR_c6; 2.
SWART; SW00005; DEATH; 1.
SWART; SW00005; DEATH; 1.
PROSITE; PS50107; DEATH DOMAIN; 1.
PROSITE; PS00185; EGF 2; 1.
PROSITE; PS50050; TNFR_NGFR_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                   62 DFCLGCAAAP-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus (Mouse)
                                                                                                                                                                                            387 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                101 WRRCR 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            196 WOPCK 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI TaxID=10090;
                                                                                                                                                                             Receptor.
SEQUENCE
                                                                                                                                                                                                                          Query Match
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us-10-062-599-59.rspt

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35; Conservative
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                             FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=1773;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=H37RV
    [2]
SEQUENCE FR
STRAIN=K1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bishai W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
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                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 10
053668
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6 LRRILLRILVLGLWLALLRSVAGEQAPG--TAP-CSRGSSWSADLDKCMDCASCRARP--- 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J., Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebaihia M., Baker S., Basham D., Brooks K., Chillingworth T., Connerron P., Cronin A., Davis P., Davis R.W., Dowd L., White N., Farrar J., Feltwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagels K., Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C., Quail M., Rutherford K., Simmonds M., Skelton J., Stevens K., "Complete genome sequence of a multiple drug resistant Salmonella enterica servovar Typhi CT18.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   27; Gaps
                                                                                                                                                                                                                   Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Salmonella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Indian citrus ringspot virus: a proposed new species with some affinities to potex-, carla-, fovea- and allexiviruses."; Arch. Virol. 145:1895-1908(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12.6%; Score 76.5; DB 16; Length 245; 30.8%; Pred. No. 4.1; ive 9; Mismatches 38; Indels 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
23kDa protein (Putative 23 kDa mucleic acid binding protein).
Indian citrus ringspot virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        59 IMMTSFTRIIIVFGLLRNALGTPSAPPNQV----LLGLALFLTFFF 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               --CLGCAAAPPAPFRLLWPILGGALSLTFVL 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=20496665; PubMed=11043949;
Mustici G., Accotto G.P., Noris E., Masenga V., Luisoni E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       245 AA; 26755 MW; C9B9931F0653A4D4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Viruses; ssRNA positive-strand viruses, no DNA stage.
NCBI_TaxID=104664;
                                                                              01-WAR-2002 (TrEMBLrel. 20, Created)
01-WAR-2002 (TrEMBLrel. 20, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
                                             245 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  222 AA.
                                                                                                                                                   Flagellar biosynthetic protein Flip
                                             PRT;
                                                                                                                                                                                                                                                                                                                                                  MEDLINE=21534947; PubMed=11677608;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL, AL627272; CAD05727.1; -.
InterPro; IPR005837; Flip.
InterPro; IPR005838; TypeIII_P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRINTS; PRO1302; TYPE3IMPPROT.
PRODOM; PD002586; TYPE1II P; 1.
TIGREAMS; TIGRO1103; TIPP; 1.
PROSITE; PS01060; FLIP 1; 1.
PROSITE; PS01061; FLIP 2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 Similarity 30.8%;
33; Conservative
                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00813; FliP; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Complete proteome. SEQUENCE 245 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          60 --HSDF--
                                                                                                                                                                                          Salmonella typhi
                                                                                                                                                                                                                                                               NCBI_TaxID=601;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Milne R.G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                Q8Z5R3;
                                       Q8Z5R3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                933060
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Matches
RESULT 8
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                      28Z5R3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           93306C
                                                                ACCOOR NAME OF THE PARTY OF THE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21 RGSQIRSVRLLP---WRPFTRFPV---CPSGTSPYSRGTHSQPSYVRCQNCERARQWFRA 74
Rustici G., Milne R.G., Accotto G.P.;
"Nucleotide sequence, genome organization and phylogenetical analysis of Indian citrus ringepot virus.";
Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF184952; AAF01114.1;
EMBL; AF406744; AAK97527.1;
SRQUENCE 222 AA; 25455 MW; 636A47058DDBDD1D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                             3 RGSLRRLLRLLVLGLWLALLRSVAGEQAP-GTAPCSRGSSWSADLDKCMDCASCRA--RP
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                                                                                                                                                                                                                                                                                                                                                 Gaps
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STRAIN-CDC 1551 / Oshkosh;
Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
Peterson J., DeBoy R., Dodson R., Gwinn M., Haft D., Hickey E.,
Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M., Salzberg S.L.,
Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Whole genome comparison of Mycobacterium tuberculosis clinical and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=98295997; PubMed=9634230;

Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris Gordon S.V., Biglmeder K., Gas S., Barry C.E. III. Tekaia F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Davies R., Devin K., Feltwell T., Gentles S., Hamlin N., Holroyd & Hernsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., Oliver S., Osborne J., Quail M.A., Rajanfream M.A., Rogers J., Sulston J.E., Taylor K., Whitehead S., Squares S., Squares R., Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;
                                                                                                                                                                                                                                                                                                                                             19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          49;
                                                                                                                                                                                                                                                                          Ouery Match 12.4%; Score 75.5; DB 12; Length 222; Best Local Similarity 35.4%; Pred. No. 4.7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12.4%; Score 75.5; DB 16; Length 449; 23.0%; Pred. No. 9.2; Live 16; Mismatches 52; Indels 49.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
                                                                                                                                                                                                                                                                                                                                             38; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     laboratory strains.";
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AL021929; CAA17338.1; ALT_INIT.
EMBL; AE006934; AAK44478.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                449 AA; 46926 MW; FCE6EF930F03D1E6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                75 HDGPRCLHQRPDYSRLQAPPDPFQHLNSFEPILLAALSV 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20, Last sequence update)
20, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                60 H-SDFCL-----GCAAAPPAPFRLL---WPILGGALSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              449 AA
                                                                                                                                                                                                                                                                                                                                          7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Putative membrane protein.
RV0246 OR MT0260 OR MTV034.12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-JUN-1998 (TrEMBLrel. 06, 01-MAR-2002 (TrEMBLrel. 20, 01-MAR-2002 (TrEMBLrel. 20,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mycobacterium tuberculosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               genome sequence.";
                                                                                                                                                                                                                                                                                                                                                 35; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nature 393:537-544(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tuberculist; Rv0246; -.
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SEQUENCE
                                                                                                                                                                                                                                   Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                      QBCXG1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3,
                        215 ALPHR--IVPRVHAAPGLHKLVYVGWTAIRTNGWYRRYLLVQVLFGSVVLGSSFHSIRVA 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MARGSLRRLLRLLVLGLWLALLRSVAGEQA -- PGTAPCSRGSS -- WSADLDKCMDCASCR 56
                                                     ----- BILGG----- 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       31 PGTAPCSRGSSWSADLDKCMDCASCRARP--HSDFCLG--CAAAPPAPFRLLWPILGGAL 86
                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 635;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  28; Indels
                                                                                                                                                                                                                                                                                                                         Gardner A., Mcmurray A.;
Submitted (NOV-1996) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                     ProDom; PD000448; Na/ntran symport; 1.
PROSITE; PS50267; NA NEUROTRAN SYMP_3; 1.
Hypothetical profein.
SEQUENCE 635 AA; 71267 WW; 2841834039D8F14A CRC64;
                                                                                                                                                                                                Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
connexin40.1 (Gap junction protein).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
12.4%; Score 75.5; DB 5;
Best Local Similarity 36.6%; Pred. No. 13;
Matches 26; Conservative 10; Mismatches 28;
                                                                                                             273 AVPGDQPDEVVAVVLFVCVGLLGGIALWNRVR 304
                                                                                               85 -----ALSLIFVLGLLSGFLVWRRCR 105
                                                                                                                                                                            635 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 370 AA
                                                                                                                                                                                                                                                                                                                                                                  EMBL; Z82083; CAB04975.1; ---
EMBL; Z81503; CAB04975.1; ---
EMBL; Z81503; CAB04975.1; JOINED.
Wormbep; ZK1010.9; CE23490.
InterPro; IPR000175; Na/ntran_symport.
Pfam; PF00209; SNF; 1.
PRINTS; PR00176; NANEUSMPORT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
Eiberger J., Soehl G., Willecke K.;
                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                   57 ARPHSDFCLGCAAAPPAPFRLLW-
                                                                                                                                                                                                                                                                                                                                           EMBL; Z81503; CAB04115.1; -. EMBL; Z82083; CAB04115.1; JOINED.
                                                                                                                                                                                     O18288;
01-JAN-1998 (TrEMBLrel. 05,
01-MAY-1999 (TrEMBLrel. 10,
01-MAR-2003 (TrEMBLrel. 23,
                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              : | : : | : 149 WMTCLVGAIIG 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 87 SLIFVLGLLSG 97
                                                                                                                                                                                                                                                     Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                 ZK1010.9 protein.
ZK1010.9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI TaxID=9606;
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018288
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9 ILIRLLVLGLWLALLRSVAGEQAPGTAPCSRGSSWSADLDKCMDCASCRARPHSDFCLGCA 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17 IMLALLRSVAGEQAPGTAPCS-----RGSSWSADLDKCMDCASCRARPHSDFCLGCA 68
              and human genome.";
Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: ONE GAP JUNCTION CONSIETS OF A CLUSTER OF CLOSELY PACKED PAIRS OF TRANSMEMBRANE CHANNELS, THE CONNEXONS, THROUGH WHICH MATERIALS OF LOW WW DIFFUSE FROM ONE CELL TO A NEIGHBORING CELL (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     143 EASNELGKVLSPIIGAAFALITWYFVFFFPVISFLCAILVFFIKERRNRQTPPP 198
                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
STRAIN=HTE831 / DSM 14371 / JCM 11309;
MEDLINE=2220767; PubMed=12235376;
Takami H., Takaki Y., Uchiyama I.;
"Genome sequence of Oceanobacillus iheyensis isolated from the Iheya
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          69 AAPPAPFRLLWPILGGALSL-----TF-VLGLLSGFLV--WRRCRRERSSPPP 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               38; Gaps
"Structural and functional diversity of connexin genes in the mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12.3%; Score 75; DB 4; Length 370; 27.9%; Pred. No. 8.6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             69 AAPPAPFRILWPILGGALSLTFVLGLLSGFLVWRRCRRERSSPP 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ridge and its unexpected adaptive capabilities to extreme
                                                                                                                                                                                                                                                                                                                                                                                                                                                    370 AA; 40140 MW; CD49F31743A7F7C2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   411 AA; 45188 MW; 589B48F6EC39275A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Mullidrug resistance protein (Bfflux transporter).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Oceanobacillus iheyensis.
Bacteria, Firmicutes; Bacillales; Oceanobacillus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         148 LLKTLLEAAFGALHYFLFGFLAPKKFPCT----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   environments.";
Nucleic Acids Res. 30:3927-3935(2002)
EMBL; AP004598; BAC13662.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
ses 29; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=182710;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      310 LVSRDAALLSQVLLRVLYMVPIAFVMVRGAESLPAMALAGPAAAVTFLAGQVAGSLIMIT 369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 52 CASCRARPHSDFCLGCAAAPPAPFRLL------WPILGGALSLTFVLGLLSGFLVWRR 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ---SWSADLDKCMD 51
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01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
101-MAR-2003 (TrEMBLrel. 23, Last annotation update)
101-MAR-2003 (TrEMBLrel 23, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.

STRAIN-ATCC 19089 / CB15;

STRAIN-ATCC 19089 / CB15;

MEDLINE-1173698; PubMed-11259647;

Nierman W.C., Feldblyum T.V., Laub M.T., Paulsen I.T., Nelson K.E., Eisen J., Heidelberg J.F., Alley M.R.K., Ohta N., Maddock J.R., Eisen J., Heidelberg J.F., Newton A., Stephens C., Phadde N.D., Ely B., DeBoy R.T., Dodson W.J., Durkin A.S., Gwinn M.L., Haft D.H., Kolonay J.F., Smit J., Craven M.B., Khouri H., Shetty J., Berry K., Utterback T., Tran K., Wolf A., Vamathevan J., Ermolaeva M., White O. Salzberg S.L., Venter J.C., Shapiro L., Fraser C.M.;

"Complete genome sequence of Caulobacter crescentus.";

Proc. Natl. Acad. Sci. U.S.A. 98:4136-4141(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             31; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                Bacteria; Proteobacteria; Alphaproteobacteria; Caulobacterales;
Caulobacteraceae; Caulobacter.
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Submitted (MAX-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Embar, All Complete proteome.
TIGS, CC0837; -.
Hypothetical protein; Complete proteome.
FROMTENCE 519 AA; 53934 MW; F37A3A52753DB53B CRC64;
                        O1-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
Pypothetical protein CC0837.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12.3%; Score 74.5; DB 16; 24.3%; Pred. No. 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            548 AA.
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SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUE=Hippocampus;
MEDLINE=22354683; PubMed=12466851;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     104 CRRERS-----SPPP 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         370 VSAEDTPDLLAISPTP 385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AE005760; AAK22822.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                       Caulobacter crescentus.
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SEQUENCE FROM N.A.
STRAIN=BALB/C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=155892;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          33;
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Q9A9X4
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RT 60,770 full-length cDNA6.";

RL Nature 420:563-7312020].

DR EMBL; ARG9831; BAG33943.1; -.

DR RMBL; ARG9831; BAG33943.1; -.

DR MGI:2182619.15 LG13.

DR INTERPRO; IPR00566; Lipocln_cytFABP.

DR INTERPRO; IPR001661; LRR.

DR INTERPRO; IPR001631; LRR. Cterm.

DR INTERPRO; IPR001631; LRR. Cterm.

DR Pfam; PF00736; EPPP; 2.

DR Pfam; PF00736; EPPP; 2.

DR Pfam; PF00736; LRRCT; 1.

DR SWART; SW00082; LRRCT; 1.

DR SWART; SW00082; LRRCT; 1.

DR SWART; SW00082; LRRCT; 1.

DR SWART; SW00089; LRR TYPP; 3.

DR PROSITE; PS002013; LR TYPP; 3.

DR PROSITE; PS002013; LR TYPICAL, 1.

DR SWART; CS00369; LRRCT; 1.

DR SRQUENCE 548 AA; 6[817 MM; 2DB303936354B958 CRC64;

QUETY MATCH

Best Local Similarity 40.4%; Pred; No. 16;

Matches 21; Conservative 5; Mismatches 24; Indels 2; Gaps 1;

ARGGRELLVLGLMLALLRSVAGEQAPGTAPCSRGSSWSADLDKCMDCAS 54

DR RGGRELLVLSTLGRCLML--QVSAKRPPERPPESCSCTRDTAFCVDSKS 57

Search completed: February 11, 2004, 10:39:21

Job time: 37 secs
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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February 11, 2004, 10:37:18 ; Search time 21 Seconds (without alignments) 229.688 Million cell updates/sec Run on:

US-10-062-599-59 608 1 MARGSLRRLLRLAULGLWLA......LSGFLVWRRCRRERSSPPPX 114

Perfect score: Sequence:

Scoring table:

328717 seqs, 42310858 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched:

328717 Total number of hits satisfying chosen parameters:

Minimum DB seg length: 0
Maximum DB seg length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Issued_Patents_AA:* Database

1: /cgr2_6/ptodata/1/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	-	Description	Sequence 59, Appl	139,	284,	22	29249	26145,	2006	31619,		31,	31,		26.		Sequence 21147, A			7	10,		Sequence 22078, A	Sequence 18195, A	231,	equence	24730	20688,	104, Ap
SUMMARIES	í.	LD	US-09-690-454-59	US-09-489-847-139	US-09-489-847-284	847	US-09-252-991A-29249	-09	-09-252-	0	-09-252-	US-09-322-409-31	09-451-527-3	US-09-322-409-26	9	US-09-252-991A-18795	US-09-252-991A-21147	US-09-199-637A-287	9-2	-09-462-	US-08-804-227C-10	US-08-804-198-4	-09-252-	US-09-252-991A-18195	US-09-996-243-231	US-09-252-991A-25290	US-09-252-991A-24730	US-09-252-991A-2068B	US-09-220-528-104
	5	<u>a</u> ;	4	4	4	4	4	4	4	4	4	4	4	4	4	4	4	4	4	4	7	~	4	4	4	4	4	4	m
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æ	Query	March	99.8	45.1	45.1	45.1	15.9	14.6	14.4	13.7	13.2	12.6	12.6	12.6	12.6	12.3	12.3	12.1	12.1	11.8	11.8	i,	ä			11.4		11.3	11.3
	3	score	607	274.5	274.5	274.5	96.5	88.5	87.5	83.5	80.5	76.5	76.5	76.5	76.5	75		•	73.5	72	72	72	ή.	70.5	7	69.5	69		69
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28223, A 37, Appl 2, Appli 2, Appli 17414, A 29956, A 29124, A 29128, A 22300, A 12, Appl 23, Appl 7, Appli 7, Appli 77, Appli 77, Appli 77, Appli		. 0
282 27, 1 1174 2299 223, 3 27, 7 27, 7		Gaps
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2822 2822 1741 11731 2999 22912 22912 2230 7	ω	. 20
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27	2	p translat re 607; D ed. No. 4.
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	Cation N: M. Rub NO: 2006F1 NO: 2006F2 TE: 20 NUMBER: 20 NUMBER: 11998- NUMBER: 1998-	sapiens ON: Xaa rity nservat
नन्नन्नन्नन्नन्नन्नन्नन्नन्नन्नन्नन्नन्	1-59 6531447 70RWATION: Steven M. St	Homo sapie SITE (114) FORMATION: 3 4-59 h Similarity 13; Conserv
68 68 . 5 68 . 5 68 . 5 68 . 5 68 . 5 68 . 5 68 . 5 68 . 5 68 . 5 67 . 5	10-454-59 10ce 59, Application US/096904 10c. 6531447. 10c. INFORMATION: 10c. The CANT: Steven M. Ruben, et al. 3 OF INVENTION: 32 Human Secr. 11 APPLICATION: 32 Human Secr. 11 APPLICATION NUMBER: US/09 12 APPLICATION NUMBER: 00/044, 12 APPLICATION NUMBER: 00/048, 12 FILING DATE: 1998-11-10 13 APPLICATION NUMBER: 00/048, 13 APPLICATION NUMBER: 00/048, 14 FILING DATE: May 30, 1997 15 APPLICATION NUMBER: 00/048, 15 FILING DATE: May 30, 1997 16 APPLICATION NUMBER: 00/048, 17 FILING DATE: May 30, 1997 18 APPLICATION NUMBER: 00/048, 18 FILING DATE: May 30, 1997 18 APPLICATION NUMBER: 00/056, 19 APPLICATION NUMBER: 00/	ORGANISM: Homo sap FEATURE: NAME/KEY: SITE LOCATION: (114) OTHER INFORMATION: 9-690-454-59 ery Match st Local Similarit tches 113; Conse
	LIT 1 19-690-454 quence 59 quence 59 quence 59 trent No. PPLICANT: PPLICANT: PRICE REFER RICHER APPL	ORGANISM: FEATURE: NAME/KEY: OTHER INFO: 9-690-454 ery Match st Local (the control of the contro
80000000000000000000000000000000000000		ORGANISM: PEATURE: NAME/KEY: LOCATION: OTHER INF -09-690-454 Query Match Best Local
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TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
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61 SDFCLGCAAAPPAAPFRLLWPILGGALSLTFVLGLLSGFLVWRRCRRERSSPPP 113
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                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: Rosen et al FILLE OF INVENTION: 98 Human Secreted Proteins CURRENT PELICATION NUMBER: US/09/489,847 CURRENT PELICATION NUMBER: US/09/489,847 EARLIER FILING DATE: 1999-07-29 EARLIER FILING DATE: 1999-07-29 EARLIER APPLICATION NUMBER: 60/095,486 EARLIER APPLICATION NUMBER: 60/095,486 EARLIER APPLICATION NUMBER: 60/095,486 EARLIER FILING DATE: 1998-08-05 EARLIER APPLICATION NUMBER: 60/095,454 EARLIER APPLICATION NUMBER: 60/095,454 EARLIER FILING DATE: 1998-08-06 EARLIER APPLICATION NUMBER: 60/095,454 EARLIER FILING DATE: 1998-08-06 EARLIER FILING DATE: 1098-08-06 EARLIER EARLIER FILING DATE: 1098-08-06 EARLIER EARLIER FILING DATE: 1098-08-06 EARLIER EA
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TITLE OF INVENTION: 98 Human Secreted Protein FILE REFERENCE: PZO31P1

CURRENT APPLICATION WHORER: US/09/489,847

CURRENT FILING DATE: 2000-01-24

EARLIER FAPILICATION NUMBER: UC/US99/17130

EARLIER FILING DATE: 1998-07-29

EARLIER FILING DATE: 1998-07-30

EARLIER FILING DATE: 1998-08-05

EARLIER FILING DATE: 1998-08-05

EARLIER FILING DATE: 1998-08-05

EARLIER APPLICATION NUMBER: 60/095,486

EARLIER PRILING DATE: 1998-08-12

EARLIER PRILING DATE: 1998-08-12

EARLIER PRILING DATE: 1998-08-12

EARLIER FILING DATE: 1998-08-15

EARLIER FILING DATE: 1998-08-16

EARLIER PRILING DATE: 1998-08-16

EARLIER PRILING DATE: 1998-08-16
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CORGANISM: Homo sapiens
US-09-489-847-284
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: AERGIGNOSA FOR DIAGNOSTICS AND THERAPEUTICS FILE REFERENCE: 107196.136

CURRENT APPLICATION NUMBER: US/09/252,991A

CURRENT FILING DATE: 1999-02-18

PRIOR FILING DATE: 1998-02-18

PRIOR APPLICATION NUMBER: US 60/094,190

PRIOR APPLICATION NUMBER: US 60/094,190

PRIOR APPLICATION NUMBER: US 60/094,190

PRIOR PILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142
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Pred. No. 1.3e-22;
1; Mismatches 0; Indels 1:
     Length 155;
  Score 274.5; DB 4; Length
Pred. No. 1.3e-22;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                   Sequence 228, Application US/09489847
Fatent No. 6476195
GENERAL INFORMATION
GENERAL INFORMATION
GENERAL INFORMATION
TITLE OF INVENTION: 98 Human Secreted Proteins
FILE REFERENCE: P2031P1
CURRENT APPLICATION NUMBER: US/09/489, 847
CURRENT APPLICATION NUMBER: PCT/US99/17130
EARLIER APPLICATION NUMBER: PCT/US99/17130
EARLIER APPLICATION NUMBER: 60/094,657
EARLIER FILING DATE: 1998-07-29
EARLIER FILING DATE: 1998-08-05
EARLIER FILING DATE: 1998-08-05
EARLIER PEPLICATION NUMBER: 60/096,319
EARLIER APPLICATION NUMBER: 60/095,454
EARLIER APPLICATION NUMBER: 60/095,454
EARLIER APPLICATION NUMBER: 60/095,455
EARLIER APPLICATION NUMBER: 60/095,455
EARLIER FILING DATE: 1998-08-06
EARLIER FILING DATE: 1998-08-06
NUMBER: OF SEQ ID NOS: 376
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; Sequence 29249, Application US/09252991A
; Patent No. 6551795
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96.4%;
Query Match
Best Local Similarity 96.4%;
Matches 54; Conservative
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ORGANISM: Homo sapiens
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US-09-489-847-228
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Best Local S:
Matches 54
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us-10-062-599-59.rai

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GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: U5/09/252,991A
CURRENT FILING DATE: 1999-02-18
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: ARRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REPERBNCE: 107196,136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-02-18
PRIOR PLING DATE: 1998-02-18
SEQ ID NO 29850
LENGTH: 249
                                           --AATPSAAACC 162
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            79 WPILGGALSLTFVLGLLSGFLVWRRCRRERSS 110
                                                                                                                              163 WGRAGVAARYAWRCGTLAGASPPTSCRRSSSS 194
                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: 1999-02-18

PRIOR APPLICATION NUMBER: US 60/074,788

PRIOR FILING DATE: 1998-02-18

PRIOR PLICATION NUMBER: US 60/094,190

PRIOR FILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 31619

LENGTH: 152
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Patent No. 6551795
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Best Local Similarity
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Best Local Similarity
Matches 40; Conserv
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US-09-252-991A-31619
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APPLICANT: Marc J. Rubenfield et al.

TITLE OF INVENTION: MUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: NUCLEIC ACID AND THERABEUTICS

TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERABEUTICS

CURRENT PAPLICATION NUMBER: US/09/252,991A

CURRENT FILING DATE: 1999-02-18

PRIOR APPLICATION NUMBER: US 60/074,788

PRIOR APPLICATION NUMBER: US 60/094,190

PRIOR PILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 26445

LIENGTH: 400
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APPLICANT: Marc J. Rubenfield et al.
APPLICANT: NOTICE AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: ABRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REPERENCE: 107196.136
CURRENT APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
ERIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
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                                                                                                                                                                                 38 WCSSTRSGGAACRRCCRASSTAPCSRASPSATAAPRTRTGSNCWAGAAPTCWSATTGRCR 97
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                                                                                                   31; Gaps
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                                                     Length 248;
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                                                                                                 23; Indels
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                                                   DB 4;
                                                                           0.0062;
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38.3%; Pred. No. 0.08;
tive 4; Mismatches
                                              15.9%; Score 96.5; D)
30.0%; Pred. No. 0.000
cive 9; Mismatches
                                                                                                                                                                                                                                                                       51 DCASCRARPHSD-FCLGCA---AAPPAPFR 76
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                                                                                                                                        18 WLALLRSVAGE-----QAPGTAPCSRGS
                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 26145, Application US/09252991A
Patent No. 6551795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 20063, Application US/09252991A Patent No. 6551795
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US-09-252-991A-26145
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                                                                    Local Similarity 30.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 14.6 Best Local Similarity 38.3 Matches 23; Conservative
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US-09-252-991A-29249
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                                              Query Match
Best Local Si
Matches 27,
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; ORGANISM: Canis familiaris
US-09-451-527-31
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US-09-322-409-26
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                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: Sin, Gek-Kee
APPLICANT: Sin, Gek-Kee
APPLICANT: Sin, Gek-Kee
APPLICANT: Dreitz, Matchew J.
APPLICANT: Wonderling, Ramani S.
TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC
TITLE OF INVENTION: CANINE AND USES THEREOF
FILE REFERENCE: IM-2-C1
CURRENT FILING DATE: 1999-05-28
BARLIER APPLICATION NUMBER: 60/087,306
BARLIER PILING DATE: 1999-05-29
NUMBER OF SEQ ID NOS: 154
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 31
LENGTH: 250
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Patent No. 6482403

GRUBERAL INFORMATION:
APPLICANT: Sim, Gek. Kee
APPLICANT: Yang, Shumin
APPLICANT: Wonderling, Ramani S.
TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC
TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC
TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC
FILE REFERENCE: IM-2-C2
CURRENT APPLICATION NUMBER: US/09/451,527
CURRENT FILING DATE: 1999-12-01
EARLIER PILING DATE: 1999-05-29
EARLIER PILING DATE: 1999-05-29
MUNBER OF SEQ ID NOS: 174
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 31
LENGTH: 250
TYPE: PRI
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  ---PILGGALSLTFVLGLLSGFLV 100
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49 RLVLAQRWMVRLQAVAGSQMQILLEAVNTEIHFVTFCAFQDTSQQLAALKPWITRRNFSG 108
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ch 12.6%; Score 76.5; DB 4; Length 250; l Similarity 27.5%; Pred. No. 0.95; 36; Conservative 15; Mismatches 47; Indels 3
                                  160 RPTFSPFRRSRSCQAAASAATPAPSATLWVLVKHRRMAAPI---SLSLT-
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58 RP----HSDFCLGCA-AAPPAPFRLLW
                                                                                                                                                                                                                        Sequence 31, Application US/09322409
Patent No. 6471957
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT ORGANISM: Canis familiaris
                                                                               101 WRRCRRERSSP 111
                                                                                                                   206 ----RTRRSAP 212
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Matches 36; Conserv
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Sequence 26, Application US/09322409
Fatent No. 6471957
GENERAL INFORMATION:
APPLICANT: Sim, Gek-Kee
APPLICANT: Vang, Shumin
APPLICANT: Parejtz, Marthew J.
APPLICANT: Parejtz, Marthew J.
APPLICANT: Wonderling, Ramani S.
TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC
TITLE OF INVENTION: CANINE AND VEES THEREOF
FILE REPRENCE: IM-2-C1
CURRENT APPLICATION NUMBER: US/09/322,409
CURRENT APPLICATION NUMBER: 60/087,306
EARLIER PAPLICATION NUMBER: 60/087,306
EARLIER PILING DATE: 1989-05-29
NUMBER OF SEQ ID NOS: 154
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 26
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                                                                                                                                                                                                                       45 DLD-KCMDCASCRARPHSDFCLGCAA--APPAPFRLLWPILGGALSLTFVLGLLSGFLVW 101
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                                                                                                    ------EQAPGTAPCSRGSSWSA 44
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Batent No. 6482403
GENERAL INFORMATION:
APPLICANT: Sim, Gek-Kee
APPLICANT: Sim, Gek-Kee
APPLICANT: Wonderling, Shumin 3.
TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC TITLE OF INVENTION: APLICANT APPLICANT: Wonderling, AMD FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC TITLE OF INVENTION: ACID MOLECULES, AND USES THEREOF FILE REFERENCE: IM-2-C2
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     5; DB 4; Length 250; 0.95;
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                                                    Indels
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Score 76.5; D'
Fred. No. 0.95; Mismatches
  12.6%;
illarity 27.5%;
Conservative 1
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Best Local Similarity 27.5%;
Matches 36; Conservative 15
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Query Match
Best Local Similarity
Matches 36; Conserv
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APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: ARRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REPERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
FUNRENT APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      135 CLELOCOPDSSTLVPPRSPGALEATALPAPQAP-RILLILL---LPVALLLMSTAWCLHW 190
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ------EQAPGTAPCSRGSSWSA 44
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                                                                                                                                                                                                                                                                                                                                                                                                    12.6%; Score 76.5; DB 4; Length 276; 27.5%; Pred. No. 1.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               15; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11 RLLVLGLWLALLRSVAG-------
CURRENT APPLICATION NUMBER: US/09/451,527
CURRENT FILING DATE: 1999-12-01
EARLIER APPLICATION NUMBER: 09/322,409
EARLIER FILING DATE: 1999-05-28
EARLIER FILING DATE: 1998-05-29
SOFTWARE: PATENTIN Ver. 2.0
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US-09-252-991A-18795
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                                                                                                                                                                                                                                                                                                                     ; ORGANISM: Canis familiaris
US-09-451-527-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                               36; Conservative
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Best Local Similarity
Matches 36; Conserv
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US-09-252-991A-18795
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                                                                                                                                                                                                                               SEQ ID NO 26
LENGTH: 276
TYPE: PRT
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59 PHSDFCLGCA-----AAPPAPFRLLW-----PILGGALSLT-----FVLGLLSGFLVWRR 103
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20 RPSTTRKPAMCSLTLWLAESTAAVPSWACSESPETLVMLRSMSWATWLCSSAAVAICWLR 79
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 305;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 12.3%; Score 74.5; DB 4; Best Local Similarity 29.1%; Pred. No. 2; Matches 37; Conservative 10; Mismatches 61;
                            FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Search completed: February 11, 2004, 10:40:26
                                                           PRIOR APPLICATION NUMBER: US/09/252,99:
PRIOR PRINT APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 21147
                                                                                                                                                                                                                                                                                                                                                              : Pseudomonas aeruginosa
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February 11, 2004, 10:39:29; Search time 34 Seconds (without alignments) 702.046 Million cell updates/sec
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Copyright (c) 1993 - 2004 Compugen Ltd.
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                                                                                                                   OM protein - protein search, using sw model
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Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                                           Title:
Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description		Semience 59, Appl	Semience 39, Appli	TIME '* SOURCE	Sequence 4, Appli	Sequence 1/8, App	Seduence 1/8, App	Sequence 3/, Appl	Sequence 444, App	Sequence 1305, Ap	Seguence 5, Appli	Sequence 5, Appli	sequence /, Appli	Sequence 7, Appli	Seguence 9. Appli	Sequence 4, Appli
SUMMARIES	ID	. US-10-062-599-59	US-10-062-831-59	US-09-742-454A-4	US-09-883-777-4	US-10-024-298A-178	US-10-042-211A-178	IIS-10-331-4968-37	118-10-295-027-444	118-10-295-027-1306	US-09-742-4542-5	US-09-883-777-5	TIS-09-742-4EAB-7	(-WFCF-3F/ CA CA LIVE - DE CA	117 100 00 001	6-1.1.1-588-60-50	US-10-251-947-4
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TYPE: PRT ORGANISM: Homo sapiens

r	ין ביותרונים יי	Sequence 2, Appli	ednence 6,	14	לן מטתפונהם		equence 13	14	'n	60,	σ	Semicondo 21 And	Somice of Appl	Sequence 31, Appl	seguence 26, Appl	Seguence 26. April	Semience 19951 A	Company of the same	Sequence 312/, Ap	Sequence 3845, Ap	Sequence 5911, Ap	Sequence 5912, Ap	Segmence 64 April	91100	Semience 1100 an	מש ירפור המוויים שלי	ddw '/87 anna	Sequence 11890, A	Sequence 6004. Ap	Segmence 5 April	Lack of enterpolation	Comission of Apple	Sequence 23/3, Ap	de '7618 amanhac	Seguence 2, Appli
10-2	-10-01-	1000	102101	-10-251-	-10 - 303 -	463-13	-10-063-	10-000-402-14	- 000-01-	0-152	0-156	US-10-262-439-31	0-216	10-01	707	10-218	10-156	0-108	C 403C-001-01	10-108-2804-384	.0-369	10-369-493-591		0-434	0-369	19-975-719-787	704 717 717 7	811-19/-951-0	-09-738-626	3-60-	-10-436-523	-10-264-049-257	-104-047-31	100000000000000000000000000000000000000	05-10-208-731-2
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ALIGNMENTS

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1 MARGSLRRLLRLLVIGLWLALLRSVAGEQAPGTAPCSRGSSWSADLDKCMDCASCRARPH 60
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61 SDFCLGCAAAPPAPFRLLWPILGGALSLTFVLGLLSGFLVWRRCRRERSSPPP 113
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 571; DB 10;
Pred. No. 5.7e-48;
0; Mismatches 6;
                                                                                                                                          Sequence 1, Application US/09742454A

Batent No. US2020041876A1

GENERAL INFORMATION: GENERAL

TITLE OF INVENTION: TWEAK Receptor

TITLE OF INVENTION: TWEAK Receptor

FILE REFERENCE: 2968-B

CURRENT APPLICATION NUMBER: US/09/742,454A

CURRENT FILING DATE: 2000-12-19

PRIOR PELING DATE: 1999-12-20

PRIOR FILING DATE: 1999-12-20

PRIOR FILING DATE: 1000-05-10

NUMBER OF SEQ ID NOS: 7

SOFTWARE: PATENTION NUMBER: 60/203,347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/09/883,777
CURRENT FILING DATE: 2001-06-18
PRIOR APPLICATION NUMBER: US 60/172,878
PRIOR FILING DATE: 1999-12-20
PRIOR FILING DATE: 2000-05-10
PRIOR FILING DATE: 2000-05-10
PRIOR FILING DATE: 2000-12-19
SEQ ID NOS: 16
SEQ ID NOS: 16
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Sequence 4, Application US/09883777
Patent No. US20020110853A1
GENERAL INFORMATION:
APPLICANT: Wiley, Stewen R.
TITLE OF INVENTION: TWEAK RECEPTOR
FILE REFERENCE: 2968-C
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Best Local Similarity 94.7<sup>3</sup>
Matches 107; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Homo sapiens
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                                                                                   RESULT 3
US-09-742-454A-4
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                                                                                                                                                                                 Length 114;
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                                                                                                                                                                          Query Match 99.8%; Score 607; DB 12; Best Local Similarity 100.0%; Pred. No. 1.6e-51; Matches 113; Conservative 0; Mismatches 0;
                   NAME/KEY: SITE

LOCATION: (114)

OTHER INFORMATION: Xaa equals stop translation
US-10-062-599-59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LOCATION: (114)
OTHER INFORMATION: Xaa equals stop translation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Steven M. Ruben, et al.
TITLE OF INVENTION: 32 Ruman Secreted Proteins
FILE REFERENCE: PZ006PI
FILE REFERENCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           THIS KEPERALCATION NUMBER: US/10/062,831
CURRENT PILING DATE: 2002-02-05
PRIOR PRING DATE: 1002-02-05
PRIOR PILING DATE: 1998-11-10
PRIOR FILING DATE: 1998-11-10
PRIOR FILING DATE: MAY 28, 1998
PRIOR FILING DATE: MAY 28, 1998
PRIOR FILING DATE: MAY 30, 1997
PRIOR FILING DATE: MAY 30, 1997
PRIOR FILING DATE: MAY 30, 1997
PRIOR APPLICATION NUMBER: 60/048,190
PRIOR APPLICATION NUMBER: 60/048,190
PRIOR APPLICATION NUMBER: 60/048,190
PRIOR APPLICATION NUMBER: 60/048,190
PRIOR FILING DATE: MAY 30, 1997
PRIOR FILING DATE: MAY 30, 1997
PRIOR PRILING DATE: MAY 30, 1997
PRIOR APPLICATION NUMBER: 60/048,101
PRIOR FILING DATE: MAY 30, 1997
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PRIOR FILING DATE: MAY 30, 1997
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GENERAL INFORMATION:
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SEQ ID NO 59
LENGTH: 114
TYPE: PRT
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Best Local Similarity
Matches 113; Conserval
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LOCATION: (114)
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US-10-331-496A-37
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LENGTH: 129
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61 SDFCLGCAAAPPAPFRLLWPILGGALSLTFVLGLLSGFLVWRRCRRERSSPPP 113
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Pred. No. 5.7e-48;
0; Mismatches 6; Indels
                                                                                                                                                                                                    PUBLICATION NO. US20030143540A1
GENERAL INFORMATION:
APPLICANT: ASAHI KASEI KABUSHIKI KAISHA
APPLICANT: AAKIO MATSUDA
APPLICANT: Goichi HONDA
APPLICANT: Goichi HONDA
APPLICANT: Goichi HONDA
APPLICANT: Goichi HONDA
APPLICANT: Winkiko NAGANO
ITTLE OF INVENTION: NF K B Activating Gene
FILE REFRENCE: 1254-0191P
CURRENT APPLICATION NUMBER: US/10/024,298A
CURRENT FILING DATE: 2003-04-08
PRIOR APPLICATION NUMBER: 60/314,385
PRIOR APPLICATION NUMBER: 60/278,641
PRIOR FILING DATE: 2001-03-26
PRIOR PULING DATE: 2001-03-26
PRIOR PULING DATE: 2001-03-26
PRIOR PULING DATE: 2001-03-26
PRIOR PULING DATE: 2001-03-26
PRIOR APPLICATION NUMBER: JP524018/2001
PRIOR PULING DATE: 2001-03-26
PRIOR FILING DATE: 2001-03-26
PRIOR PULING DATE: 2000-12-28
PRIOR PULING DATE: 2000-13-28
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TITLE OF INVENTION: NFKB Activating Generile Reperator: 1224-0122P
CURRENT APPLICATION NUMBER: US/10/042,211A
PRIOR APPLICATION NUMBER: US 2000-40228B
PRIOR FILING DATE: 2000-12-28
PRIOR FILING DATE: 2001-03-26
PRIOR FILING DATE: 2001-03-26
PRIOR FILING DATE: 2001-03-26
PRIOR PRILING DATE: 2001-03-26
PRIOR FILING DATE: 2001-03-26
PRIOR APPLICATION NUMBER: US 60/278,640
PRIOR FILING DATE: 2001-03-26
                                                                                                                                                                                     Sequence 178, Application US/10024298A
Publication No. US20030143540A1
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Matches 107; Conservative
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ORGANISM: Homo sapiens
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#### APPLICANT: ZHANG, ZEMIN
#### TITLE OF INVENTION: TEREATHENT OF TUMOR
#### CURRENT APPLICATION NUMBER: US 60/345,444
#### PRIOR PLING DATE: 2002-12-30
### PRIOR PAPLICATION NUMBER: US 60/345,444
### PRIOR PILING DATE: 2002-01-02
### PRIOR PELING DATE: 2002-01-02
### PRIOR PELING DATE: 2002-01-25
### PRIOR PELING DATE: 2002-03-25
### PRIOR PELING DATE: 2002-03-25
### PRIOR PELING DATE: 2002-03-05
### PRIOR PELING D
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Pred. No. 5.7e-48;
0; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                       93.9%; Score 571; DB 12;
94.7%; Pred. No. 5.7e-48;
11ve. 0; Mismatches 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 37, Application US/10331496A Publication No. US20030228305A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SPENCER, SUSAN D.
WILLIAMS, P. MICKEY
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94.7%;
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Best Local Similarity 94.7%;
Matches 107; Conservative
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APPLICANT: HILLAN, KENNETH J.
APPLICANT: PHILLIPS, HEIDI S.
NUMBER OF SEQ ID NOS: 182
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 178
LENGTH: 129
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Best Local Similarity 94.7°
Matches 107; Conservative
                                                                                                                                  TYPE: PRT
ORGANISM: Homo sapiens
US-10-042-211A-178
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ZHANG, ZEMIN
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Ginsberg, Wendy M.
Gish, Kurt C.
Glynne, Richard
Hevezi, Peter A.
Mack, David H.
Aziz, Natasha
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Publication No. US20030232350A1

SABREAL INFORMATION:

APPLICANT: Afar, Daniel

APPLICANT: Afar, Daniel

APPLICANT: Ginb. Knit C.

APPLICANT: Ginb. Knit C.

APPLICANT: Ginb. Knit C.

APPLICANT: Marcay, Reidy M.

APPLICANT: Marcay, Reidy M.

APPLICANT: Marcay, Reidy M.

APPLICANT: Marcay, Richard

APPLICANT: Marcay, Richard

APPLICANT: Warray, Richard

FILIS DATE: 2002-11-13

PRIOR PAPLICATION NUMBER: US 60/336, 666

PRIOR RILING DATE: 2001-11-13

PRIOR APPLICANTION NUMBER: US 60/347, 313

PRIOR APPLICANTION NUMBER: US 60/347, 211

PRIOR APPLICANTION NUMBER: US 60/347, 211

PRIOR PRILING DATE: 2001-11-29

PRIOR PLILNG DATE: 2001-11-14

PRIOR PLILNG DATE: 2001-11-24

PRIOR PLILNG DATE: 2001-11-29

PRIOR PLILNG DATE: 2001-11-29

PRIOR PLILNG DATE: 2001-11-29

PRIOR PLILNG DATE: 2001-11-39

PRIOR PLILNG DATE: 2001-11-39

PRIOR PLILNG DATE: 2001-11-39

PRIOR PLILNG DATE: 2001-01-08

PRIOR PLING DATE: 2002-01-10

PRIOR PLILNG DATE: 2002-01-10

PRIOR PLILNG DATE: 2002-02-13

PRIOR PLILNG DATE: 2002-02-13
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                                                        61 SDFCLGCAAAPPAPFRLLWPILGGALSLTFVLGLLSGFLVWRRCRRREKFTTP 113
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61 SDFCLGCAAAPPAPFRLLWPILGGALSLTFVLGLLSGFLVWRRCRRERSSPPP 113
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93.9%; Score 571; DB 12; Length 129;
Best Local Similarity 94.7%; Pred. No. 5.7e-48;
Matches 107; Conservative 0; Mismatches 6; Indels
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Sequence 1305, Application US/10295027

Publication No. US20030232350A1

GENERAL INFORMATION:

APPLICANT: Afar, Daniel
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US-10-295-027-444
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1 MARGSLRRLLRLLVLGLWLALLRSVAGEQAPGTAPCSRGSSWSADLDKCMDCASCRARPH 60
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APPLICANT: Marray, Richard
APPLICANT: Marray, Richard
APPLICANT: Watson, Susan R.
APPLICANT: Eos Biotechnology, Inc.
AITLE OF INVENTION: Methods of Screening for Modulators of Cancer
TITLE OF INVENTION: Methods of Screening for Modulators of Cancer
CURRENT APPLICATION NUMBER: US 09/663,733
PRIOR PLILOR DATE: 2002-11-13
PRIOR PLILOR DATE: 2000-09-15
PRIOR PLILOR DATE: 2001-11-15
PRIOR PLILOR DATE: 2001-11-15
PRIOR PLILOR DATE: 2001-11-15
PRIOR PLILOR DATE: 2001-11-21
PRIOR PLILOR DATE: 2001-11-21
PRIOR PLILOR DATE: 2001-11-29
PRIOR PLILOR DATE: 2001-11-21
PRIOR PLILOR DATE: 2001-11-21
PRIOR PLILOR DATE: 2001-12-14
PRIOR PLILOR DATE: 2001-12-14
PRIOR PLILOR DATE: 2001-12-14
PRIOR PLILOR DATE: 2001-12-14
PRIOR PLILOR DATE: 2002-01-06
PRIOR PLILOR DATE: 2002-01-06
PRIOR PLILOR DATE: 2002-01-10
PRIOR PLING DATE: 2002-01-10
PRIOR PLING DATE: 2002-01-10
PRIOR PLING DATE: 2002-02-13
PRIOR PLING DATE:
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Best Local Similarity 94.7%; Pred. No. 5.7e-48;
Matches 107; Conservative 0; Mismatches 6;
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; Sequence 5, Application US/09742454A
; Patent No. US20020041876A1
; GENERAL INFORMATION:
    ATILE OF INVENTION: TWEAK Receptor
; TITLE OF INVENTION: TWEAK Receptor
; FILE REFERENCE 2968-B
; CURRENT APPLICATION NUMBER: US/09/742,454A
; CURRENT FILING DATE: 2000-12-19
; PRIOR FILING DATE: 1999-12-20
; PRIOR FILING DATE: 2000-05-10
; PRIOR FILING DATE: 2000-05-10
; RICHARD FILING DATE: 2000-05-10
; NUMBER OF SEQ ID NOS: 7
; SOCTIMARE: Patentin Ver. 2.0
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US-09-742-454A-7
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                                                                                              FEATURE:
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                                                                                                                                                                                                            0; Gaps
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                                                                                                                                                                                                                                                                 61 SDFCLGCAAAPPAPFRLLWPILGGALSLTFVLGLLSGFLVWRRCRRERSSPPP 113
                                                                                                                                                                                                                                                                                         61 SDFCLGCAAAPDAHFRLLWPILGGALSLVLVLALVSSFLVWRRCRRREKFTTP 113
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                                                                                                     74.0%; Score 450; DB 9; Length 129; 75.2%; Pred. No. 3.2e-36; ive 6; Mismatches 22; Indels
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75.2%; Pred. No. 3.2e-36;
iive 6; Mismatches 22;
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Patent No. US20020041876A1
GENERAL INFORMATION:
TITLE OF INVENTION: TWEAK Receptor
FILE REFERENCE: 2968-B
FILE REFERENCE: 2968-B
CURRENT APPLICATION NUMBER: US/09/742,454A
CURRENT FILING DATE: 2000-12-19
PRIOR FILING DATE: 1999-12-20
PRIOR FILING DATE: 1999-12-20
PRIOR RILING DATE: 1999-12-20
PRIOR FILING DATE: 2000-05-10
PRIOR FILING DATE: 2000-05-10
SOFTWARE: PATENTIN NUMBER: 60/203,347
                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INCORDATION:
APPLICANT: Wiley, Steven R.
TITLE OF INVENTION:
FILE REFERENCE: 2068-C
CURRENT FILING DATE: 2001-06-18
PRIOR FILING DATE: 1099-12-20
PRIOR FILING DATE: 1999-12-20
PRIOR FILING DATE: 2001-06-19
PRIOR PLING DATE: 2000-05-10
PRIOR PLING DATE: 2000-05-10
PRIOR PLING DATE: 2000-05-10
PRIOR PLING DATE: 2000-12-19
SOFTWARE: PALENTIN VERSION 3.1
SOFTWARE: PALENTIN VERSION 3.1
                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 5, Application US/09883777 Patent No. US20020110853Al
                                                                                                                      Best Local Similarity 75.2
Matches 85; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 75.29
Matches 85; Conservative
               ; TYPE: PRT
; ORGANISM: Mus sp.
US-09-742-454A-5
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; ORGANISM: Mus sp.
US-09-883-777-5
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US-09-742-454A-7
LENGTH: 129
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                                                                                                       Query Match
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                                                                                                                                                                                                                                                                                                                                                            1 MARGSLRRILIRILVLGIMIALIRSVAGEQAPGTAPCSRGSSWSADIDKCMDCASCRARPH
                                                                                                                                                                                                                                                                                                                    22; Gaps
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                                                                                                                                      OTHER INFORMATION: Description of Artificial Sequence: human TWEAK OTHER INFORMATION: receptor fusion protein construct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 SDFCLGCAAAPPAPFRLLWPILGGALSLTFVLGLLSGFLVWRRCRRERSSPP 112
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ) OTHER INFORMATION: Human TWEAK receptor fusion protein construct US-09-883-777-7
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                                                                                                                                                                                                                                               Query Match
71.2%; Score 433; DB 9; Length 309;
Best Local Similarity 74.1%; Pred. No. 3.5e-34;
Matches 83; Conservative 2; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GRUERAL INCOMMATION:
APPLICANT: Wiley, Steven R.
TITLE OF INVENTION: TWEAK RECEPTOR
FILE REFERENCE: 2968-C
CURRENT APPLICATION NUMBER: US/09/683,777
CURRENT FILING DATE: 2001-06-18
PRIOR FILING DATE: 1999-12-20
PRIOR FILING DATE: 2000-05-10
PRIOR FILING DATE: 2000-05-10
PRIOR FILING DATE: 2000-05-10
PRIOR FILING DATE: 2000-12-19
NUMBER: OF SEQ ID NOS: 16
SEQ ID NO 7
SEQ ID NO 7
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APPLICANT: Wiley, Steven R.
TITLE OF INVENTION: TWEAK RECEPTOR
FILE REFERENCE: 2969-C
CURRENT APPLICATION NUMBER: US/09/883,777
CURRENT FILING DATE: 2001-06-18
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Patent No. US20020110853A1
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SEQ ID NO 7
LENGTH: 309
TYPE: PRT
ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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Best Local Similarity 74.18
Matches 83, Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9; Gaps
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PRIOR APPLICATION NUMBER: US 60/172,878
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: US 60/203,347
PRIOR APPLICATION NUMBER: 2000-05-10
PRIOR APPLICATION NUMBER: PCT/US00/34755
PRIOR PILING DATE: 2000-12-19
PRIOR PILING DATE: 2000-12-19
PRIOR PLING DATE: 2000-12-19
PRIOR PLING DATE: 2000-12-19
NUMBER OF SEQ ID NGS: 16
SOFTWARE: Patentin version 3.1
SEQ ID NO 9
LENGTH: 300
LENGTH: 300
PYPE: PRI
ORGANISM: Artificial Sequence
FEATURE:
FRATURE:
CORGANISM: Artificial Sequence
FEATURE:
COTHER INFORMATION: Human TWEAK receptor fusion protein construct
US-09-883-777-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-10-251-947-4

Sequence 4, Application US/10251947

Sequence 4, Application US/10251947

Publication No. US203009990A1

GENERAL INFORMATION:

APPLICANT: Hsu, Hailing

TITLE OP INVENTION: TALL-1 Receptor Molecules and Uses Thereof

TITLE OP INVENTION: TALL-1

CURRENT APPLICATION NUMBER: US/10/251,947

CURRENT FILING DATE: 2002-09-20

NUMBER OF SEQ ID NOS: 14

SEQ ID NO 4

LENGTH: 171

TYPE: PRT

CRGANISM: Homo sapiens

US-10-251-947-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ouery Match 62.4%; Score 379.5; DB 10; Length 300; Best Local Similarity 88.0%; Pred. No. 5.2e-29; Matches 73; Conservative 0; Mismatches 1; Indels 9;
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